GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	Ś	;	Length 1604	1	Description 035021 Mycobacteri	acteri
- nucleic search, using sw model	2 6 4			1 MF043540 1 MBDR351 1 AE006921	U43540 Mycobacteri U35017 Mycobacteri AE006921 Mycobacte	acteri acteri obacte
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	ACCESSION	U35021	0.1.1.7	9243		
	KEYWORDS	. 120021.	1 61:1049243	744.5		
	SOURCE	Mycobac	terium bov	vis BCG.		
	ORGANI SA	Bacteri	a; Firmic	utes, Actinobact	ceria; Actinobacteridae;	
		Actinom	ycetales; terium; My	Corynebacterine ycobacterium tub	Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.	
em_htg_othe	REFERENCE	l (bas Mahaira	1 (bases 1 to 1604) Mahairas, G.G., Sabo, P	604) abo, P.J., Hickey	/, M.J., Singh, D.C. and Stov	er, C.K.
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	TITLE	Molecul bovis B	ar analysi CG and vir eriol. 178	is of genetic di rulent M. bovis 8 (5), 1274-1282	Molecular analysis of geneile differences between mycobacterium bovis RCG and virulent M. bovis J. Bacteriol. 178 (5), 1274-1282 (1996)	
SUMMARIES	REPERENCE	96200099 2 (base	(buses 1 to 1604)	604) abo b 1 Hickey	96200093 2 (bases 1 to 1604) Washiran C., Saho D. Hirkey M.J. Singh.D.C. and Stover.C.K	er, C.K.
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ADVEDAJ RLVOGDI TDAELVSQLVAESDAVVHFAAESHVDNALDNPEPFLHTNVIGTF
TI I. FAVRRHGVRLHHI STDEVYGDLELDDRAFFTESTPYNPSSEPYSATKAGADMLVRA
WYSSLCVRAT I. SNCSNNYGRYGHVEKFI PRQITNCLTGLLKLYGDGGNVVRMIHVDDH
NSA VRR I. LDRGRI GETYLI SSEGERONLTVLRSLLRIMDRDPDDFDHYTINRVRHILRY
AJ DPSRI, YDELCWAPKHTDFERALKTI IDWYRDNESWLASLKHAGGRYGDAGO"
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lundrquvgsyssaxurglefraldpepsaxvytoxsgsvptovytoirecsptpgrwds
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stycgcpslsprdaaapsfeedvrrglllpggtdvsrrigemrgt"
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WVRSLCVRATISN/SNNYGPYQHVEKFIPRQITNCLTGLLKLYGDGGNVR/MIHVDDH
NSAVRRILDRGRIGETYLISSEGERDNLTVLRSLLRLMDRDPDDFDHVTDRVAHDLRY
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ADVEDATRIVGGDTTDAELVSQLVAESDAVVHPAAESHVDNALDNPEPFLHTNVIGTF
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/note="3-4 copies in M. tuberculosis genome; Found in the rtb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv. H37Rv. Erdman, and many isolates; not found in M. smegmatis & M. avium."
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1 (bases 1 to 928).
Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K Molecular analysis of genetic differences between Mycobacterium bovis BCG and virulent M. bovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
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/gene- "IIIC"
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/protein_id="AAB66647.1"
/db_xref="G1:2326949"
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/transl_table-11
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/qene="rmlC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhamnose biosynthetic genes related to a novel repeated sequence of Mycobacterium tuberculosis
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Namku, Taegu
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Namku, Taegu
                          Hickey, Molecular Microbiology, Ave. W., Seattle, WA 98119, USA
                                                                                                                                                                                 /note="site of deletion breakpoint in this organism. Virulent M. bovis has additional 10 kbp at this site" 637~\rm c 416 g 214~\rm t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
Bacteria; Firmicuttes; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology,
Medicine, Yeungnam University, 317-1, Daemyungdong,
705-035, South Korea
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      Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, M. Pathogenesis Corp., 201 Elliott Ave. W., Location/Qualifiers
                                                                                                /organism="Mycobacterium bovis"
/sub_species="RGG"
/db_xref="taxon:1765"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="This region contains an authentic point mutation, causing a premature stop, and is not the result ol a sequencing artifact; similar to SP:P16431 GB:X17506 PID:41684 PID:882614 GB:U00096; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gill,J., Mikula,A. anu pismath...

Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers

1. 9764

1. 9764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Defendant R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Wilnn, M., Hall, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Unayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                            /organism="Mycobacterium bovis"
/db_xref="taxon:1765"
misc_difference replace(1400. -29281,")
/note="absent in related avirulent strain M. bovis BCG"
count 1706 a 3191 c 2929 g 1453 t, 2 others
Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology,
Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA
Location/Qualifiers
1. .9281
                                                                                                                                                                                                                                                                                                                                           Gaps
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section 7 of 280 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridac; Actinomycetales; Corynebacterineae: Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 9764)
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/strain="CDC1551"
/db_xreff"taxon:83331"
                                                                                                                                                                                                                                                                                         Length 9281;
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                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                           Score 18; DB 1;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="clinical strain"
122. .1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity; putative"
1449. 2123
/gene="MT0096"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:13879142
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ilarity 100.0%;
Conservative 0
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete genome.
AE006921 AE000516
AE006921.1 GI:138
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE006921
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SOURCE
ORGANISM
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                                                                                                                                                                                                       BASE COUNT
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AUTHORS
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                          JOURNAL
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Forcein_id="Aak44323.1"

Aboxere="601:13879147"

/t.canslation="MAVTVGVICALPOELAYLRGVLVDAKROOVAQILEDSGULAAHR
vvi.AaaGMGKVNTGLTATLJADRFGCRTIVFTGVAGGIDPELCIGDIVIANHVVGHINF
coll-10PERLENPOPCHIPPETTPERCOTYDDAVLIDRYHRRIDGFTLANI.STPAKINGGN
copriyGTLLTGDOYLHCEFTRENELHELGGMAVEMEGGAVQOICASFDIPWILVIRAL
SDLAGADSGVDFNRFVGEVAASSARVLLRELLPVLTAC."
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/product="methyltransferase, putative"
/product="methyltransferase, putative"
/product="methyltransferase, putative"
//ib_xref="cl:13879144"
//ib_xref="cl:138
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VWHCT.RCGDFALGGPGGRGAPEDAPI.MRGRALROATITRALGVERI.VKAI.VLAAAW
AVMERGARGATI.NRII.VVLRAACKEVDOMTVITALI.KAI.ARKPSTI.AT.ITGMI.A
AYAVI.QAVEGVGI.MILKRWERYFAVVATSTFLPLEVIIII.AKGITTTRVVTFSI.NVAAV
VYII.ISKRLPGVRGGRKAYDVERRGEGLDLERAAMI.T"
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/protein_id "AAK443±±1"
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/drox ref="G1:14879146"
/drox ref="G1:14879146"
/drox ref="G1:14879146"
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// ranslation="MSVYKHAPSRVLRQTRSTVKGRSGSTSWRRVFTGD"
// ranslation="MSVYKHAPSRSTKG"
// ranslation="MSVXKHAPSRSTKG"
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nucleosidase/S-adenosylhomocysteine nucleosidase,
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/protein_id-"AAK44321.1"
/db_xret-"G1:13879145"
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/qene="MT0099.1"
3/91. .4162
/qene="MT0099.1"
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  5105. .7390
/yene-"MT0101"
5105. .7390
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/qene-"MT0100"
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/gene="Mr0100"
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/qene="MT0099"
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/gene-"MT0099"
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                                                                                                                                                                  5105. .7390
/gene-"MT0101"
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/qtme-"MT0098"
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/acne "MT0098"
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VSGTVSGRAVRVGKPSWIGSSSCHPNWRAARRHAESI GETAVEVUSDEEPCGVI AVAD
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LRDRGHYVAAWGDGI TUNGPALLARADLGMA TGRGTDVAI JGAAD I ILVROHLDVVPLALD
LARATMRTVKLNMWWAFGYNI AAI PVAAAGLLNPL VAGGAAMAFSSFFVVSNSLRLKKF
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/db_xref="GI:JB$79149"
/tb_xref="GI:JB$79149"
/translation="MLAQATTAGSFNHHASTVLQGCRGVPAAMWSEPAGAIRKHCAT1
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/db_xref="G1:13879150"
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                                                                                                                                                                                                                                 AJAAVLEVPVADLSVWEGVVPATRETGWQWVLSALALPVVTWAAWPFHRVAMRNARHH
AASMETLISVGITAATIWSLYTVFGNHSPIERSGIWQALLGSDAIYFEVAAGVTVFVL
VGRYFEARAKSQAGSALRALAALSAKEVAVLLPDGSEMVIPADELKEQVRFVVRPGQI
                                                                                                                                                                                                                                                                                                           VAADGLAVDGSAAVDMSAMTGEAKPTRVRPGGQVIGGTTVLDGRLIVEAAAVGADTQF
AGMVRLVBOAQAQKADAQRLADRISSVFVPAVLVIAALTAAGMLIAGGQPDRAVSAAL
AVLVIACPCALGLATPTAMMVASGRGAQLGIPLKGYKSI.EATRAVDYVVFDKTGTLTT
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RPVVPPVGRLGTRRAPRRQHSPMTWRRMALLCVGTAQTALGTVQGFGLDVGLTHQHPT
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STTRILTHLPVVIGAVLAIMVWRSASGPRPRPDAVAAEPUIVI.PDNASKGRRKGHLMP
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GKLGQHNGLPVSIVVTTTLTDLQTGAGKGFTGGGTLLIPMADV1RWTSHAHHYSPASGR
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TGRTDITELTLACGPDNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQPRTNTFHHPERF
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/translation="MTTAVTGEHHASVQRIQLRISGMSGSACAHRVESTLNKLPGVRA
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/note="similar to SP:P46840 PID:559912: identified by sequence similarity; putative"
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/protein_id="AAK44324.1"
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/gene="MT0103"
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AUTOMIS BY LOGI-"MKESMKSGSFATGLAMMLAPMVAAPGLAAADPATKPVDYQQLTD
VVLARGLSQRGVPFSWAGGG ISGPTGTGGTNTVGEDASGLLUYAYAGAGIKLPRSG
GOMYKVU,ROQAAKGGILI PY GPTGTGGTOVALLGGGMLEVGDVVVSFVFTNGMT
GOMYK VILNOVASKENGAKESKRESKRESKRESKGARPTGGGTTGAGTASARFAKNAMT
FAANSLRHKALTITVVFLAFSFPFRASCFPLLSARSRRLWWVN
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WESKLFAFTINVCPPDAGPLVPFGVNYYYPVWWGGIGAAIATAVIGPFVSHLKGWYM
                                                                                                                                                               putalive 8 amino-7-oxonomanoate synthase (bioF), putative dethiobiotin synthetase (bioB) genes.
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Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clouding, sequencing, and identification of Mycobacterium bovis BCG biotin blosynthetic genes by complementing two Mycobacterium
                                                                                                                 adenosylmethionine-8-amino-7 oxononanoate aminotransterase (bioA),
18-JAN-1998
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1 (bases 1 to 10019)
Yu, S. and Jacobs, W.R. Jr.
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/note "ORE2; similar to MrcY336.36"
/wwich Start 1
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/note-"ORFL; similar to MTCY336.37"
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           BCT
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/db_xref="G1:2791845"
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     AF041819 10019 bp DNA
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/sub_species "BCC"
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/product-"unknown"
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/чепе≖"bioA"
1810. .3123
/чепе="bioA"
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neftapemlighlisvlavvasalmwgmrehrgpgmvaglsjglttaaataaggalvv
rikygaldfdyvplskgdialtyvtgappvefarrplotaltumpagtaslvyalla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    видъ. .9406
/note."ORF10; similar to MTCY336.13c"
/codou_start-1
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/note="ORF11: similar to MTCY336.12"
/codon_start-3
                                                                                                                             /note-"BioB; similar to MTCY336.15c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTEARDDLGGYPAVDPSSNARTEALETPQAPVS"
                                                                                                                                                                                                                                                       /product-"biotin synthetase"
/protein_id-"AAB96962.1"
/db_xref="G1:2791851"
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Stover, C. Kendall and Mahairas, G.G.
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/product="unknown"
/protein_id="AAB96963.1"
/db_xref="G1:2791852"
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/product="unknown"
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186264
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/qene-"bioh"
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CGPHLAPAPMANSLPGQWTAHVTI.ARRVGGHQI.GRAI.RI.AGRPSRII!RIFAGI.RRWNG
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CLYRRIPAOHTLINQLDTQASEEELGGTLCCALANRIRTTRODAN IN ADAADLGPR
RALTREPLAPOLTATATAGQGGLGAHIKV LKALFRPPARKGGCVHIPVSRESRPGRG
SRSISSRRAGPLRAPAGHGLATPHKRPTKPQTRHHPEQPAIKHVTAKWLPDPPS
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative 8-amino-7-oxononanoate synthase"
/protein_id="AAB96957.1"
/db_xref="G1:2791846"
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GLLFSSGYTANLGAVVGLSGPGSLLVSDARSHASLVDACKLSRAKVVYTPHKDVDAVD
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RODDLAEVGCRLAGYTQLAGARYDQABABAAABHGAMALLARND. VYH.LIADLDHPG
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VSCAGLVJGSWPDPPGLVAASNRSALARIATVRALPAGAASLDAGDFAAMSAAAFDR
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GELOGHGEPYSIVYTTTLIDLDGTGARGFTCGGTLLAMBANY RMTSHAHYSPASGR
YPQAIFDHGTPLALYHTKLAPAQRIMLFANDRGCTKPGCDAPAYHSOAHHYTGWTS
TGRTDITDLTLACDPDNRLARKGWTTRKNTHGHTEMLPPPHLDHGQPRTNTFHHHEKL
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GLYEEGGLAGRADDVWITTLSKALGSGGVVLGEPTVRAHLIJONARPF FDTGLAPAAV
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LLLGQDWRTRITELAAGLTAGLDTARALPAVTDVRVCGAIGVIECDRPVDLAVATPAA
LDRGVWLRPFRNLVYAMPPYICTPAEITQITSAMVEVARLVGSLP"
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/note="ORF7; similar to MYCY251.13c"
/codon_start=1
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/gene="bioD"
4277. .4957
/gene="bloD"
/mote="bloD; similar to MTCY336.33c"
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/note="ORFG similar to MTCY336.32c"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                        /note="BioF; similar to MTCY336.34c"
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/codon_start=1
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/db_xref="G1:2791850"
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                                                                                         3120. .4280
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GLARVIKEHANDEGRQLLEQLTEMTTVDAVIRMAGRDMGDFLIDEPLEDILSTPEVSHY
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CSIGNI TABOVIJOLAAROVIHRININIETARSFRANVYTHTWEERWOTI,SMVRDAGME
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VAAFRI ALPPEMI,RFAGGRE TTLGDLGARROILGGI NAVIJT FLGRPAEADLELIDELOMPLKALINASE.
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    SKSTSSRRAGPLRPAGHGLATPRRRPHRHRTRPQTRHHPEQPATRHHVTAKWLPDPPS
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                                                                                                                                                                                                                          /note "similar to GP:1680650; identified by sequence similarity; putative"
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.2997. .3236
.2997. "MY1625"
.Acto. "MY1625"
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/codon_start-1
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complement (3955, .4054)
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/transl_table=11
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/qene-"ME1626"
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1947. .2996
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RALTGEPLAPOLTATATAOROGLIGHAHIKVIRALFRPPARGGCVIIPPGKRSRPGRO
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, M., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzbergy, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Whole genome comparison of Mycobacterium tuberculosis clinical ar
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Submitted (25-APR-2001) The Institute for Genomic
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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QLRVTDEFAALRPPGQL"
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/protein_id="I38801
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MAGANADELPTOFHPTMLFAGRAGGRPLITPBAT IGEBCAILUDROGNET TAGVHPMG
DLAPRDVAAALDARIKATGDPCVX LDARGIEGFASRFPTVTASCRAAGIDPVRQVIP
VVPGAHYSCGGIVTDVYGQTELLGLYAAGEVARTGLHGANRLASNSLLEGLVVGGRAG
KAAAAHAAAGRRAAFSSATWPEPISYTALDRODLQRAMSRNASMYRAAAGLHRACDS
LSGAQVRDVACRDBEDVALTLVAQSVTAAALARTESRGCHHRAEYPCTVPEQARSIV
VRGADDANAVCVQALVAVC
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GAGARLDESVPGRWALTREGGHSRRRIVHAGGDATGAEVQRALQDAAGMLDIRTGHVA
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FGDTKLGSAVPTPPVLIVQAVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSL
HPLSAPMTLRWLTDRFAGKPLTDHRVRTTWPTIFNPMTYAGMARLAVIAAKVITGRKL
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/gene="MT1631"
/gene="MT1
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/db_xref="GI:13881260"
                                                                                                                                              complement(5660. .6193)
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/gene="MT1630"
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/gene="MT1632"
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/gene="MT1632"
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/gene="MT1630"
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Mycobacterium tuberculosis and uses thereof
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Sequence | from patent US 6224881.
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Riley, L.W. and Chong, P.
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TKQITGLFLAVYLMANITOGSST TANOPVHOPMQIYET EMEMBERTH HILLSOFTAND TOWN TO THE TANOPVHOPM TEREST TANOPVHOPMQIYET EMEMBERTH TANOPVHOPMQIYET FOR TANOPVHOPMQIYET FOR THE TANOPVHOPMQIYET FOR THE TANOPVHOPMANITOGY A NCCMAMVVAVASDIGFNKY LLGLSPKTPEFRRGMLY AINPVCFCSLILLAAGLSIVTFY CGGAALQPYSPLVAIYTALVMPPLLAAATKGKYY LRRTHDGIDLPMYDEHONPSAAV CTCHVCHQDFERPDMLACQTHGAHVCSLCLSTDKQAEHVLPGLARAHIFGLOVP" COMPLIGMENT (3485. 4378)
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/db xref "G1:18
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/product="DNA-directed RNA polymerase, alpha subunit"
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/ARTESDLLDIRNFGQKSIDEVKIKLHQLGLSLKDSPPSFDFSEVAGYDVATGTWSTEG
                                                                                                                                                                                                                                                                                                                /LTAINS I AT 100 * "MMPGV1TNSESPTAADHDRITATRETLEDYTLRLAPRSYRRWPP
AVOGT SALGGTAYLADFA1GANVGTTWGTAANLCGTALFALVVVTVCLULAYYAARYN
11) LDL 17RGGGFGYTGSVTWVIFATFTFTFTFTEFALGGSIMAQGIRLALHIPJMAGYACS
11) I FPLVVVCMKVI,SGLGJMTTPLMLILMAAPFGYILVVSHPDSIGGFFSYGGRGDGH
G1.SFGSVLLAAGVTLSLLAQIAEQ1DYLRFMPPRTPENANKWWTWTLLAGGGWVAFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MSLTRKPPRSPPORPPRISGVVRLRLDIAYDGTUFAGWAAOVGO
NFTVAGDIDAALTTIPRTPVRLRAAGRTDAGVHASGOVAHVDVPADALDNAYPRAGHVG
DPELFLILRRIGKFILPADVK ILDITRAPAGFDARFSALRRHYVRLSTAPYGVEDQOA
NYTWAWPRELDIJAWATAASHOLMGI JIDPAAFCRHREGATTI NDIQUKLIWASKAGTILVTA
ILVTADAFCWSWVKSLVGALLAVGEHRRATTWCRELLITATGRSSDFAVAPAHGITTLIQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"similar to SP:P07649 GB:X02743 PID:41718 GH:U00096
PID:1788657; identified by sequence similarity; putative"
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/note="similar to SP:P81288; identified by sequence
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                                                                         by Glimmer2; putative"
                                                                                                                                                                                          /product-"hypothetical protein"
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/gene="MT3563"
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/qene="MT3563"
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                                                                         /note-"identified
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/!ransl_table-11
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                                       /qene~"MT3561"
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LSPLFGSKAIDLCHVGPGRISPSCHIDDYIPYTTQAASFVVQRLRAGSVPH
LPGSVPQLDGSVLQMFGTAAAPAPESLHGR"
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DDHIAAIALFGNPSGRAGGLMSALTPQFGSKTINLCNNGDPICSDGNRWRAH.GYVPG
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                                                                                                                                                   Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodoson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Closes I to 16384)
Fleischmann, N.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-ARR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to SP:000298; identified by sequence similarity; putative" /codon_start=1
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Firmicutes; Actinobacteria; Actinobacteridae;
                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/protein_id="AAK47898.1"
/db_xref="GI:13883391"
                                                                         Mycobacterium; Mycobacterium tuberculosis complex. (bases 1 to 16384)
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1624. .1863
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96. .839
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871. .1566
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/gene="MT3561"
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AUTHORS
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REMARK
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                                                                                                               /traislation="MARYTGEVTRKSRRLKTD1.VGGDOAFEKRPYPPGQHGRARIKES
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complement(2729. .7503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MARLVGVDLPRDKRMEVALTY1FGIGRTRSNEILAATGIDRDLR
TRDLTEEQLIHLRDYIEANLKVEGDLRREVQADIRKKIEIGCYQGLAHRKGMPVRGQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to GP:2104383; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                /note-"similar to SP:P45812; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.18; Score 16.4; DB 1; Length 16484; 94.48; Pred. No. 1.3e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEF21A3 32096 bp DNA INV 25-UC
Caenorhabditis elegans cosmid F21A3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota: Metazoa: Nematoda: Chromadorea: Rhabditida:
Rhabditoidea: Rhabditidae: Peloderinae: Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to SP:P45810; identified by similarity; putative" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="ribosomal protein S13"
/protein_id="AAK47906.1"
/db_xref="G1:13883399"
                                                                             /protein_id="AAK47904.1"
/db_xref="G1:13883397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7129. .7503)
/gene="MT3567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(7719. .7832)
/gene="MT3567.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(7719. .7832)
/gene="MT3567.1"
                                                                                                                                                                                                                                           complement(6706. .7125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKTNARTRKGPKRT I AGKKKAR'
                                                                                                                                                                                                                                                                                                       similarity; putative"
    similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity; putative"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table-11
                                                                                                                                                                                                                                                             /gene="MT3566"
                                                                                                                                                                                                                      /gene="MT3566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="MT3567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 11346 ACGTCAAAGTGATTCGCG 11363
                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 acatcaaagtgattcgcg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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/Lrānsialion="MTRINIVIETSSLAVCTYSQTMTKTIIDFCSPSEPNSCGFGGKC
MELSLGNRCFCPFGLMGKRCQRPCQDYKSCARMKSEBRCHWTRPISTPFADMYALSC
GQCKNNGKQCALALPPILDHIEMFVGRWESKTSAHHRPPEPPNSGPYKETLDVUTSFVP
SFDRPPVNISYRAFTLGTDYHVBFGFLTSRFPHEDYGFVELMRPDFGDADAS
NTGLMLIEGCTVKGTQIRLETKYKKGMAGVFRBEIVKSKRMFNLINANSLEEKVVWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The true left end of clone F2IA3 is at 1 in this sequence. The true right end of clone F2IA3 is at 6434 in sequence 281071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The end of this sequence (31993, 32096) overlaps with the start of sequence 281071.
                                                                                                                                                                                        Direct Stabilission
Submitted (06-NOV-1996) Nematode Sequencing Project, Sander Centre,
Intraton, Cambridge CB10 1Kg, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sander.ac.uk or revensinglede.wustl.edu
                                                                                                                                                                                                                                                                                                                                                On Jul 24, 1997 this sequence version replaced gi:1695020.
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The true left end of clone F28F8 is at 31993 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone F21A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both
The C.eleqans Sequencing Consortium. Fractional Ipublished errata appear in Science 1999 Jan 1;28,5(538):35 and 1999 Mar 26;283(548):3;285(5483):1493]]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /crganism."Cacnonhabditis elegans"
/db_xref-"Laxon:6239"
/chromosome-"V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zare - F21A3.Ll"
Znote-"CAT Mot M-LENA
Znote-"CAT Mot M-LENA
predicted using LRNascan-SE-1.11
preliminary prediction
similar to (kNA-Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted using tWMAscan-SE-1.11
prediminary prediction
similar to tWMA Val"
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/db_xref="G1:3876159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(216, .288)
/qene."F21A4.t2"
/note "CAC Val V tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (21%, 1288)
/qene="F21A3.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dene-"F21A3.11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone-"F21A3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               available information.
                                                                                                                               10 32096)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .32096
                                                                                                                                   2 (bases 1 to
MCMurray, A.A.
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gene

CDS

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/rodon_start_1
/rodon
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Actinowycetales; Corynebacterine tuberculosis complex.

1 (bases 1 to 3247)
1 (bases 1 to 3247)
2 (bases 1 to 3247)
3 (bases 1 to 3247)
4 (bases 1 to 3247)
5 (bases 1 to 3
                                                                                                                                                                                                  PEFTIKVEQQ IDVDVWFDTALRIFAKILKVAK EBQEKLLEKLEVKGGAW PKGPRAGAO
TSTVAYNG TIDDFY KTVCSGRPAWALHWRDVMLDWDKLLENTFFFSKMFFAY EKHQKS
LETSERBEKLQATKEHYTVWKNHFEFEMAKNQAATVEYLMPEEFAKEEFTDKKKDPEE
                                  INNHYPFMYVRIKAGIPTLHDILKCLSSDKMSYTTASFLAVDMISAIETLSASGWYLRN
PDSKOWMLDIKTROFYLADATDITVSSDKRHRAIDETHLRTAESIDLHWKTGDLIYAP
RSFYDROGSHRMTELDMMEMMLYVLYDWTHGKLPWKSSKSRERIMEMKELFIENLOKE
                                                                                                                                                                                                                                                                                                                                                                   EAAAAVVGKKRRGRKPKKEDDPKMELKDEVKDLKDFVVEGTQVTEFSKSRLHMSGKRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(27870, .28389,28450, .28539,28591, .28708,
29358, .29580))
/qrue="F21A3.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comptoment(join(27870. .28389,28450. .28539,28591. .28708,
29358. .29580))
/qene="F21A3.6"
GAAYCYI,VCDKPCKKFG11,YLE1GEDNVTT1ANQVDFYHQOSS1,GYSHKFSAL,1DAG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"predicted using Genefinder
Weak similarity to Shark myoglobin (SW:P02206), contains
similarity to Pram domain: PF00042 (Globin), Score-39.5,
E-value=1.5c-10, N*1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2001
segment 70/162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.4; DB 3; Length 32096; Pred. No. 1.5e+02;
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Mycobacterium tuberculosis H37Rv complete genome;
295586 AL123456
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PPFINCRNWNCREARYAGKLANCG1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>.</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /qene- "F21A4.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21379 AFATGAAGIGATROGG 21996
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Matches 17; Conservative
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26204. .26320,27040. .27510)
/gene="F21A3.5"
join(22967. .23146,23217. .23582,24576. .24916,26030. .26153,
26204. .26320,27040. .27510)
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/gene="F21A3.4"
join(21375. .21425,21480. .21710.22206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(21375, 21425,21480, 21710,22206, 22348,22411, 22695)
/gene="P2143.4"
/note="predicted using Genetinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:017828"
/translation="mnrnrkGHDLENIEHRFTDEDLAGLKEQKLFNGKW11LEKKEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MDIKVIREKITUTTSITSESVAFYEHDVDECCRLLEHKLELEME
KKLOLSNRIDDVOSGYTELMDRYDRARRESDISGRYTAMACHLSEWMEVKLKAKM
GTHTELSATICASICESTLABETGESLLAEKRVIVQRNREEIDYRRHLINGQLKDKLDCDREEE
KCTYMINGAALDEKVYEMIKEGERVEEFKREUDECKRMLEELEMLLKKTGKKR
OILDENANLVASFSSLTEESS"
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/db_xref="GI:3876155"
/db_xref="GI:3876155"
/db_xref="SPTRENBL:017825"
/db_xr
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HEHSYERLWPYYNRTYYNGTRHPYVDPPAPVH11TGSAGCRENTUVFVEHPPPWSAVR
STDYGFGVMRVYNSTHLNFKQ1NVAQEGK1UDDFWVVKSSPKHHRFFKHRULKRLRTY
GTH1PKHHCHHKSHCDKTRRRKHISRHSHIVE!"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOMCNIKWEWLTLLIMSASLDLSFGFLVIPPRYQPVIAGYSLGILNGFGVPLRVMYYI
CVVQIAGVTVSVCALFETRFFLLYAKOSCWKHLRRPWLILNYTICVVYMIPTYLSIPD
CYTGRAYQFSKYPCLPOEVYDEKVFLLTTWSTGYAYMSLINTAVOUTLIFVFLIYWNM
RKSWVEVKRKRTDMHRFTFKTILIQVIPLITVMGPLAINFFTITVNSYYNGGANU
SISMMATHGLVSSLAMIYLHKSYWATLLQILSPKFIFEDREFMMFSKYNGHNOGOFS
complement (john (15549. 15743,15934. 16071,16247. 16444,
16540. 16599,16681. 16823,16995. 17181,17233. 17415,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(15549. 15743,15934. 16071,16247. 16444,
1640. 16598,16681. 16823,16995. 17181,17233. 17415,
17532. 17703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:017826"
/translation="MCMNTSPAKFLDTPQFLSTTMYTITIIGLPVHIFGGLCVVFKTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity to Aspergillus acid phosphatase (TR:Q12546) cDNA EST yk3q4.5 comes from this gene cDNA EST yk69fi0.5 comes from this gene cDNA EST yk23lfi3.5 comes from this gene cDNA EST yk285c4.5 comes from this gene cDNA EST yk553e5.5 comes from this gene
                                                                                                                                                                                                                                                                                                    /note="predicted using Genefinder
contains similarity to Pfam domain: PF01604 (71M
chemoreceptor), Score=254.2, E-value=5.6e-73, N=1"
                                                                                                                                   Join(14078. .14402,14665. .15074,15212. .15475)
/gene=F21A3.1"
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                            Joun(14078. .14402,14665. .15074,15212.
/gene="F21A3.1"
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similarity to protein kinases"
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/gene="F21A3.2"
/note="predicted using Genefinder
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/db_xref="GI:3876157"
/db_xref="SPTREMBL:017827"
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/db_xref="G1:3876158"
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/db_xref="G1:3876156"
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                                                                 CDS
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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old peen renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G is an increase in the observed/expected third position G is initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribusonme binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEDY PGARALI DHYRYPKLERREPTVLEVRHDLEPTSTRDGCTSGFFVENT I INCTYGDVD
APRT IALAGGSHAEHWLTALDLLGRHHFKVVTY LKWGCPLSTEEVPLI MGNNAPYPO
APRT IALAGGSHAEHWLTALDLLGRHHFKVVTY LKWGCPLSTEEVPLI MGNNAPYPO
CHWOVAAMAKLVADHEDV VETTSTRPWN IKPGDWPATYVG INGYFADNN I PVLAMR
DTPWLVKDGOPF I PADCLAKGGNPGSCGI AREKKVLVIKNP'I I.DFVAHFPLLKPLDMSD
ALCRTDTCRAVEGNVLVY ROSHHLTPTYMRTMT SELGKQI AANTIWW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Rv1565c, (MrCy336.48), len: 729. Unknown membrane protein, some similarity to 005402 HYPVFHETICAL 72.2 KD protein, from B. subblis (634 an) opt: 44 K(): 4.8c-17; PROTEIN from B. subblis (634 an) opt: 44 K(): 4.8c-17; protein in H.influenzae. N-terminal half hydrophobic. protein in H.influenzae. N-terminal half hydrophobic. FASTA results, Y392_HREIN P43993 hi0392 (245 an) opt: 265; EC): 5.5c-10; 28.3% identity in 247 an overlap. TBparse score is 0.930".
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LVAVPHVWFGRVGGVDVFLALSGFFFGGK LIRAALNPDLSLSPIAEVIRLIRRLLPA
LVAVLAGGALLTIATOPQTRWBAFANDROSLASLGYVONWELASTVSNYLRAGEAVSPLO
HIWSNSVOGGFTLLTLVAGGAYLLRRLFRGPRAPYLRTMYVLLSTLTLASFIYAI
VAHHXYQATAYYNTFARAWELLAGALVGAVVPHVRWPWMLRTAVATAALAAILSCGAL
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YSWYLWHWPLLIFWLSYTGHRHANFVEGAAVLLVSGLLAYLTTRLVEDPLRYRAPAGV
RSPAAVPPIPWRLRLRRPTIVLGSVVALLGVALTATSFTWREHVIVQRAAGKELSGLS
                                                                                                                                            Submitted (11-JUN-1998) Submitted on behalf of the Hycobacterium submitted (11-JUN-1998) Submitted on behalf of the Hycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                              Notes:
Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                            On Jun 27, 1998 this sequence version replaced 91:2117233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycobacterium tuberculosis H37kv"
/strain="H37Rv"
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/strain="H37kv"
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/protein_id="CaB09072.1"
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Nature. 393 (6685), 537-544 (1998)
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/gene="Rv1565c"
complement(39, .2228)
/gene="Rv1565c"
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/clone="Y48"
33. .32091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:8332"
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1. .32437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Y336"
complement(39.
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                                                                        (bases 1 to 32437)
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                                                                                                                   Parkhill, J.
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                                                                                                                   AUTHORS
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/translation="managedecoliavddahluhipyssigreavspvvavahda
Mitlindgopievldamsswwtaihghphldoalttydkuhinhymegelihepank
Mitlindgopievldamsswwtaihghphldoalttydkuhinhymegethepank
Telansigdphiggmphlydlaaovpraaknahluhinhymegerhedanav
Vepvvogaggmrhuppklaaovprapopphyphphymegerhedalaav
Vepvvogaggmrhuppklaaovprapopphymegerhedaltaavs
Inligopmrtriedaltaachtranskupavtdykogaloviegerhanniacavsvasve
Inligopmrtriedaltaachtranskupavtdykogaloviegerhanniacavsvasve
Inligopmrtriedaltaachtranskupavtdykogaloviegerhanniacavsvasve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firster "KATSTAN (MILY146.15c), bioA, ten: 447. Function: Firstable advence; The thionine-8 animo-7 exponentates comming transfer asset (Mil. 6.1) 006622. Contains similar tenses class-III pyridoxal-phosphate attachment sile (PS00600). FASTARESULS, BIOA_MYCLE P4548 (4.86 aa) opt: 2534; E(): 0; 85.18 identityin 436 aa overlap. Also similar to other M. tuberculosis proteins e-q. MINCY2Z, 12c, (449 aa). FASTA score: E():3.5e-16; 29.5% identity in 421 aa overlap. TBparse score; 8():3.5e-16; 29.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"SPTREMBL:006623"
/translation-"MVTMTSWPSRLFAFTDNVCPPDACPLVPEGVNYYIYPVMMGGIG
AALATAVIGPEVSMLKGWYMSFWPLISIAVITVTSIAGYAJAGFSEKYWH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probably exported has QOAPV repeats at C-terminus, similar
                                                                                                            to hypothetical M. leprae protein, to putative invasins 1.2(007390, 007391) from M. avium and slightly similar to creminus of Listeria invasion-associated protein p60 precursor p60_LISMO P21171. FASTA results, 04654 6054 DBIT BITTO (2466a) opt: 957 E(): 0: 70.0% identity in 207 aa overlap, TBparst scoreis 0.890"
                       /dvine-"Rv15660"
/hote-"Rv15660; (MTCY336.37), len: 230. Fun tion: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote-"Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3030. 3036)
/note-"possible RHS, AAGGAGG, for Rv1566c"
complement(3258. 3263)
/note-"ASNI site: ATTAAT; probably linking fraqments
[84/G6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00600 Aminotransferases class-III
pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /iransl_table II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xrcf="SPTREMBL:006624"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /qene-"Rv1567c"
complement (3259. .3543)
complement(2327. .3019)
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/transl_tuble=11
                                                                                                                                                                                                                                                                                                                                               /transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /qene= "Rv1567e"
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                                                                                                                                                                                                                                                                                                                  /codon_start- |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4791. .5104
/qene-"bioA"
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Aaiplirgirndbralavglavlalralvlpwllaravgaeaaaqkeafplvntass
Llitagltltafaitqpvvnlepgvtinavpaafavvlialfvwittklhavsqaagfl
Mldnglaataflltagvplivelgasldvlfavivigvltgrrrifgdanldklrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /i.ems.lation."mswiladaquig;wwgaplytightroykarwegracallopwr
bilkgo.cocojtpagttiveraapvivagtelliaalaplyatgspilpsadleavvg
biltighcotaltiladiptgtspegabgaserttabatbeptilladatavfall;ppsadleavvg
ristoctavalaculadataviluviviviviyivivaetgrlepvinyathileltwaheamulet
prilalvewaaghmiltytilalianletemgiagaapatbyltgvvavaakvatlavillavillaterdeavelaki,rlekypellagsliadalaavtaavtaanfetyga"
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Dorteur Roux, 75724 paris Cedex 15, France B-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1405752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /yene."hycl)"
//wene."Rv0084, (MTCY251.02), len: 316,hycb, similar to living. ECOLT Pl6430 formate hydrogenlyase subunit 4 (307 aa) living. ECOLT Pl6430 formate hydrogenlyase subunit 4 (307 aa) FASTA scores, opt: 570, z-score: 591.6, E(): 2.1e-26, (33.8% identity in 305 aa overlap) and NUOH.ECOLI opt: 237, z-score:220.7, E(): 9.5e-06, (26.5% identity in 260 aaoverlap).
                                                                                                                                                   Details of M. Luberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) (DS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Kroqh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position 6 the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /_oce="Rv0085, (MTCY251.03), len: 220. hycp, similar to
//note="Rv0085, (MTCY251.03), len: 220. hycp, similar to
splp77524|HYFE_ECOLI HYDROGENASE-4 COMPONENT E (216
aa),FASTA scores: opt: 204 z-score: 272.1 E():1.2e-07;
25.5% identity in 216 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon day, quy, or tqy) which is preceded by an upstream ribosome binding site sequence (optimally 5-13pp before the initiation codon). It this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mycobacterium tuberculosis H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .38380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:83332"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rransl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start.-1
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/qene-"hycP"
967. .1629
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/gene="hycP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .35889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation codon.
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                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /traislation="wkaatqariddsplawldavqrorheaclrrclrprpavateld
Lasndylglsrhpavidggvalringagargsrlvygdyklhdofbelaefevgaa
Gllesggytaangavglsgpgglljsbarbaslvdacklsrakvyvrphrdydav
aalbsbegravyvrphrdydsygbarshaslvdacklsrakvyvrphrdydav
LASLBSGRAVVYTDSVFSABGSLAVRELLEVCRHGALLIJDBABGLGVRGGRG
LLYELGLAGAPDVWTTTLSKALGSOGGVVLGPTPVRAHLIDAARPFIFDTGLAPAAV
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1 (bases 1 to 38380)

1 (bases 1 to 38380)

2 (bel.S.T. Brosch.R.) Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S. V., Eiglmeier, R., Gas, S., Barry Ill, C.E.,
Fekaia, F., Badcock, R., Devlin, R., Feltwell, T., Gentles, S.,
Fonor, R., Davles, R., Devlin, R., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.
Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAARAALRVLOAEPWRPOAVLMHAGELARMCGVAAVPDSAMVSV1LGEPESAVAAAAA
CLDAGVKVGCERPPTVPAGTSRLRLTARASLNAGELELARRVLTDVLAVARR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
                                                                                                                                       /note="Rv1569, (MTCY336.34c), bioF, len: 386. Function: probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class.II pyridoxal-phosphate attachment site (PS0059). FASTA results, BIOF_MYCLE P45487(385 aa) opt: 1971; E(): 0; BO.1% identity in 381 aa overlap. Also similar to 393 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTCY251 38380 bp DNA BCT 0.4-AUG: 2001
Mycobacterium tuberculosis H37Rv complete genome; segment 5/162.
274410 AG:123456
274410.1 GI:3261600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.1%; Score 16.4; DB 1; Length 32437; 94.4%; Pred. No. 1.5e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00599 Aminotransferases class-II
pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:006621"
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Nature. 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB09068.1"
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/transl_table=11
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6258. .6938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5806. .5835
/gene="biof"
                                                                                           5101. .6261
/gene="bioF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98295987
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
MTCY251/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
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VERSION
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                                                                                                       CDS
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CDS

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tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.uc.uk on Jun 27, 1998 this sequence version replaced gi:2104370.
                                                                                                                                                                                                                                                                                                                                                                           /translation-"MDQPWNANTHYDALLDAMVPLGTOCVLDVGCGDGLLAARLARRI
PYVPADIDAPOLLAKOGTREANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
PALSRIGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
PPQTLHELRSHVRALLDGACIRRLLYGRVLVTWRAPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.295390 AL123456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
/note="Rv0089, (MTCY251.07), len: 197. unknown, some /note="Rv0089, (MTCY251.07), len: 197. unknown, some similarity to sple1299-lender-CLL BIOTIN SYNTHESIS PROTEIN BIOC. (251 aa). FASTA Scores: opt: 202 z-score: 62.0 E(): 45e-07; 39.0% identity in 118 aa overlap".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Hote-"Rv0090, (MTCY251.08), len: 256. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6147. .6152
/note-"aaggaq, potential rbs upstream of Rv0090"
6158. .6928
/qene="Rv0090"
6158. .6928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="hypothetical protein Rv0090"
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Mycobacterium tuberculosis H37Rv
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/qene-"Rv0090"
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Best Local Similarity
Matches 17; Conserv
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                                                                                              /yeural "yeo086, (MTCY251.04), oxidoreductase, len: 488, /note="MY0086, (MTCY251.04), oxidoreductase, len: 488, hyco, most similar to splp74371HYFF ECOLI HYBOGENASE-4 COMPONENT FEE 1. (526 aa), FASTA scores: opt: 948 component in 17.0 for 17.0 for 35.9% identity in 493 aa overlap. Also similarto E. coli 49087711 & NUOL. ECOLI P33607 nadh dehydrogenaseichain 1 (613 aa) FASTA scores, opt: 360, derstap), and to NUON. ECOLI P33608, nadh dehydrogenase ichain n (425 aa), FASTAScores, opt: 375, z-score: 371.4, E(): 3.9e-14, (25.0% identity in 432 aa overlap).
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/gene="Rv0088"
4605. .5279
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5436. .6029
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                                             1629. .3095
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LTAATRANPOPVSESTLOTH KRGPTLGTPGAPQLLINDPLAGAESAWATCDSDNGGSTT
VVVGTPAEDSSAAVLTARAH ITVATESGSPTYLLYGGRRAVVDLADPAVVWALKLQGRV
PHVVAASTLANAVPEATRI TAPRTRGGGRASVGLPGFTVGGVVRTTRASGDEYYVVLED
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GRAVTFILGVTWTPAQUGAARVAFIJAGSGPPVPLGGVPVTIJAQADGRGFALDAVTIJPG
RSAYVAARSIJSOGGTGTRYIJVTDTGVRFAIHDDDVAHDIGIPFAALIPAWPVIATIJPS
                                                                                                                                                                                                                                                                 GAALAYAVDYKNAY I VAAAGNIGGAAQCPPQAPGYTKIJSYTYAVSPAWYDDYYLTVGS
VNAQGEPSAFTLAGEWYDVAATGEAVTSLSPFGDGTVNRLGGGHGS I PLSGTSYAAPY
VSGLAAL I KARFPFITTARQVMOR I ESTAHHIPPAGWIPLVGNGTVDALAAVSSUSI IPOA
GTATSDPAFVAVPVPRKSTPGPSDKRALHTAFAGAA I CLLALMATI ATASKRI RPGRN
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/translation "mispaytymanysgyrfil.rriffalledivgaatgalraftsl.
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                                                                                                                                                     PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGAGURVAVIDTGVA
RHRRLPRVVAGGDYVFTGDGTADCLAHGTLVAGIIAAAPDAGSDNFSGVAPDVILIISI
                                                                                                                                                                                                                           KOSSSKPAPVGDPSSTGVGDVDTMAKAVRTAADLGASVINISSIACVPAAAAPDDRAL
                                                                      /db_xref-"sptrEMBL:006316"
/translation-"mtTsrtLRLLVVSALATLSGLGTPVAHAVSPPFIDERWLPESAL
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unknown but similar to Rv3895c WTCY15F10.17 (FASTA score:
1.6e-27; 36.4% identity in 475 aa overlap); possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane spanning region near N-terminus, and to yet4967|MLK18628|l6 Mycobacterium leprae cosmid 1620; (481 ad) opt. 708 2-score: 710.9 E(): 4.5e-32; 42.98 identity in 480 ad overlap, also similar to kv3869 (MPV027.04)"
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complement(4049, .4081)
/gene-"Rv3450c"
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/yene="Rv3450c"
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/qene="kv3449"
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ARMAVLLAGLSPRLPPALNPDDADALPTTDRLTTRANRADANLTSI.LAAFAASAT IGA
IGANVATIG HIRSSMGTALAAVTGALLLLARKSADTRRSLVFA IGG ITTVATAFTVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAALDTTARPÕCORTTRLSGALAASCITAGGGLMI.VKNAI KTNVTKYSIVATAGVVAAA
GLAALLFAVIACRTYRDPIAGLTLSVIATIFGAVAGI.LAVPGVKGVIISVI.VAAMAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Rv3448, (MTCY77.20), len: 467 aa. Unknown membrane protein, contains PS00402 Binding-protein-dependent
    been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                       initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transport systems inner membrane comp signature. Some similarity to ALO21930/MTV035_1B Mycobacterium tuberculosis (472 aa) fasta score, opt: 429 -sscore: 488 4 E(): 1.1e-19; 28.2%identity in 479 aa overlap"
                                                                                                                                                                                                                                                                 an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Rv3448"
/note="PS00402 Binding-protein-dependent transport
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/strain="H37Rv"
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/product="hypothetical protein Rv3449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             systemsinner membrane comp signature" 78. .1481
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1478. .2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:8332"
/clone="Y77"
78. .1481
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1. .43401
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1478. .2845
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78 164
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LSPLFGSRADLGCNPTDPICHVGPGNEFSGHIDGYIPTTTQAASFVVQRLRAGSVPH
4706. 4723
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Mammalia; Eutherla, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="NT2R83"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
precursor cells after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                                                                                                                               /note="Rv3452, (MTCY13E12.05), len: 226. Function:
probable cutinase precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2001
                                                                                                                                                                                    /note="PS00155 Cutinase, serine active site, GGYSQG"
5165. .5168 "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone_lib:NT2RP3 clone:NT2RP3002701.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 1; Length 43401;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AK027649 3125 bp mRNA PRI 1
Homo sapiens cDNA FLJ14743 fis, clone NT2RP3002701.
AK027649
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                                                                                                                                                                                                                                                                 /gene="Rv3452"
/gene="Rv3452"
5178, see
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Isogai,T. and Otsuki,T.
Direct Submission
                                                                                                                                                                 4706. .4723
/gene="Rv3451"
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/gene="Rv3452"
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94.48;
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VERSION
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TITLE
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Pred. No. 1.8e+02;
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/note="unnamed protein product"
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induction."
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Matches 16; Conserv
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2, 2002, 22:49:09 ; Search time 366.19 Seconds (without alignments) 42.142 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930621 seqs, 428662619 residues
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	BCG deletion regio	Mycobacterium tube	M. tuberculosis ce	DNA for M. tubercu	Human EST-derived	Human ORFX ORF2359	Human cDNA seguenc	Human secreted pro	Enterococcus faeca	H. pylori flagella	II. pylori flagella
		ΙD	AAT33537	AAQ89200	AAT33656	AAV18647	AAH99048	AAC76804	AAH17859	AAA16623	AAX13377	AAT67421	AAT68027
		DB	17	16	17	19	22	21	22	21	20	18	18
		Query Match Length DB ID	12412	1535	1535	1535	2642	2753	3125	3262	10594	639	1731
	œ	Query Match	100.0	91.1	91.1	91.1	88.9	88.9	88.9	88.9	85.6	82.2	82.2
		Score	18	16.4	16.4	16.4	16	16	16	16	15.4	14.8	14.8
		Result No.	1	7	3	4	S	9	7	80	6	10	-

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Riley LW;
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                                                             This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 other deletion regions (see AAT3355) and AAT3355) have also been detected identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of an avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the presence or absence of deletion junctions (see AAT33538-46), or by detecting the presence or absence of the sequences contained within heletion pollonarides are used as contained within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis DNA sequence encoding mammalian cell entry
Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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                                                                                                                                                                                                            Deletion polypeptides are used as components of
                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 17; Length 12412; 100.0%; Pred. No. 2.1;
                                                                                                                                                                                                                                             Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
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                                            Example 1; Fig 3; 66pp; English.
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                       bacterial infection
                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                the deletion.
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                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The Ah sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced Ah sequence is in AAR71931.
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                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                       Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cellular uptake; cell entry; macrophage; passive immunisation; vaccine; gene Lherapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                   Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product - macrophage survival protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                                                                                                                                                                                                                                          UB 16;
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886..1535
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Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          91.18;
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW02301.
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Mismatches

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02-AUG-2001
17;
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  Matches
                                                                                  AAH99048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
 invasive clones. The DNA includes 2 separate coding regions (see also AAT3867-58) coding for the cell entry (AAW02302) and macrophage survival (AAW02303) proteins. It can be used to produce the cellular uptake proteins used as vaccines or to facilitate uptake of other
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-ineoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
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                                                                                             DB 17; Length 1535;
                                                                                                                                                                                                                                                                        DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                 indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                              Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                 1;
                                                                                                                                                                                                                                                                                            Cellular uptake protein; vaccine; infection; ds
                                                                                                                                                                                                                                                                                                                                                                  /note= "stop codon not given"
                                                                                            Score 16.4; DE Pred. No. 12; 0; Mismatches
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1..1534
                                           materials, e.g. therapeutic genes.
                                                                                                                                                                                                             AAV18647 standard; DNA; 1535 BP.
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                                                                                              91.18;
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                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
                                                                                                                                                                                                                                                      (first entry)
                                                                                              Query Match 91.1
Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                  AAV18647;
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    SSSSSX
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Score 16.4; DB 19; Length 1535; Pred. No. 12;

91.1%; 94.4%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel
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                                                                                                                                                                                                                                                                                                                                  Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; doq; sea urchin; expressed sequence tay; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; qene therapy; nutrition; ss.
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                                                                                                                                                                                                                                                                                              Human EST-derived coding sequence SEQ ID NO: 905.
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22;
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J, Werhman T;
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Pred. No.
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                                                                                                                                                            ВР
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A, Zhang J,
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100.0%;
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03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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18
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  1 acateaaaqtgatteged
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Drmanac RA,
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Best Local Similarity
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03-AUG-2000;
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AAC76804
1D AAC70
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Pred. No.

100.0%;

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thrombosis; contraceptive; ss
                                                                                                                 02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                       31-MAR-2000; 2000WO-US08621
                                                                                                               99US-0127607
       (first entry)
                                                                                                                                         Shimkets RA, Leach M;
                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                 WPI; 2000-602362/57.
P-PSDB; AAB42595.
                                                                                       WO200058473-A2
                                                                                                              31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                Homo sapiens.
       08-FEB-2001
                                                                                               05-OCT-2000
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; thrombolytic; immunosuppressant; immunosuppressant; antivitabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy
                                                                                                                                                                                                                                                                                                                                      Human, open reading frame, ORFX; detection; cytostatic; hepatolropic;
vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprolective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antianaemic gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthrits; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autocimunue disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyrold;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to enhance
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                                                                                                                                                                                                                 Human ORFX ORF2359 polynucleotide sequence SEQ ID NO:4717
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AAC76804;
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Length 2753;

DB 21;

88.9%; Score 16;

Query Match

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The present invention describes primer sets for synthesising 5602 [111]-length cubas defined in the specification. Where a primer set comprises: (a) an oliqued primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides, or (b) a combination of an oligonucleotide comprises a least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Where the oligonucleotide which comprises a 1'-end sequence of an oligonucleotide sequence 3'-end sequence 15'-end sequence 3'-end sequence 15'-end sequence 15'-end sequence 16'-end 16'-end
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                           Caps
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, Otsuki T;
                         Indels
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Wakamatsu A, Nagai K,
  red. No. 22;
Mismatches
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                           Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                            Human; secreted protein; immunestimulant; immunesuppressant; virucide; antibacterial; antifungal; cytostatic; antinflammatory; dermutological; antidabetic; antiasthmatic; antiarthritic; antirheumatic; projozoacide; antithyroid; immune deficiency; severe combined immunedeliciency; SCID; infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; asthma; Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia glavis; insu;in dependent diabetes mellitus; graft-versus-host-disease; autoimmune inflammatory eye disease; allergy; ss.
                                                                                                                                                                                                                                                                                                  Human seareted protein clone pt332_1 nucleotide sequence SEQ 1D NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating, preventing or ameliorating medical conditions in humans
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopoiesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity
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                 Length 3125;
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               88.9%; Score 16; DB 22;
100.0%; Pred. No. 22;
ive 0; Mismatches 0
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Agostino MJ,
                                                                                                                                                                                                AAA16623 standard; cDNA; 3262 BP.
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                 88.98;
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98US-0099229
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                                                                                                    Best Local Similarity 100.
Matches 16; Conservative
                                                                                 2 catcaaagtyattcgc 17
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Clark HF, F
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30-APR-1999
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                   Query Match
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immunodelicienty (STID), as well as viral, bacterial, Iungal and other intections. These infections include human immunodeficiency virus (HIV), herpeaviruses, mycobacteria, Leismania spp., malaria and candidiasis. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic upus crythomatosis, the und old atthritis, autoimmune pulmonary inflammation, duillain-Barre syndrame, antoimmune thyroiditis, insulin dependent diabetics mellitus, myasthenia quavis, graft versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to
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                               which the protein is preferentially expressed, as molecular weight, markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined
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   tissues in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune inflammafory eye disease. The proteins can also be used to treat affective conditions, such asthma. AAA16698 to AAA16774 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes for the human secreted proteins from the present invention.
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animals. The polynucleotides can be used as markers for
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Pred. No.
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Best Local Similarity
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associated protein.
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binding compound; bacterfum; life cycle; activator; bacteria; inhibitor;
duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
                       S
of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcus!
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                        Length 10594;
                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_except= (pos:514..516, aa:xaa)
/transl_except= (pos:524..515, aa:xaa)
/transl_except= (pos:526..528, aa:xaa)
/transl_except= (pos:535..537, aa:xaa)
/transl_except= (pos:544..546, aa:xaa)
/transl_except= (pos:550..552, aa:xaa)
/transl_except= (pos:550..552, aa:xaa)
/transl_except= (pos:550..552, aa:xaa)
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                                                                                           Sequence 10594 BP; 3197 A; 1733 C; 2323 G; 3337 T; 4 other;
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                              pylori flagella-associated protein ORF 19557055.aa.
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/transl_except= (pos:505..507,
                                                                                                                      Score 15.4; DB Pred. No. 57;
                                                                                                                                           0; Mismatches
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                                                                                                                         85.68;
94.18;
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95US-0487032
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                                                                                                                                            Conservative
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                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                flagellum; ds
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07-JUN-1995;
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                                                                        infection
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                                                                                                                                                                                                                    RESULT
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homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypoptide production, e.g. in R. coli hosts.
The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori lite cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 5679) was determined from overlapping conties generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori and igens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic, vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
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"no stop codon given"
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Pred. No. 82;
0; Mismatches
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88.9%;
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9508-0487032
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Matches 16; Conserv
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infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 5579) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8;
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88.9%;
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Matches 16; Conserv
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Sequence 96109 BP; 28783 A; 18910 C; 20341 G; 28075 T; 0 other;

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The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atheroselenosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thrombosmbolism and pulmonary embolism Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPs shown in the specification.
                                                                                                                                                                                                                                                                                                         Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McCarthy JJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids comprising single nuclectide polymorphisms, useful in applications such as forensies, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= "single nucleotide polymorphism"
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 Length 96109,
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Score 14.8; DB 22;
Pred. No. 1.7e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                           Human gene single nucleotide polymorphism #1697.
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                                                                                                                                                                                                                                                                                                                                                         pulmonary embolism; paternity test; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/*tag= a
                                                                                               Db 14162 acatcaaaatgattctcg 14179
   82.2%;
88.9%;
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2000US - 0225724
                                                                                                                                                                             AAF96936 standard; DNA; 21
                                                                  1 acatcaaaqtqattcqcg 18
                                                                                                                                                                                                                                            (tirst entry)
   Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catqiil M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST
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16-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Variation
                                                                                                                                                                                                            AAF96936;
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Family 11 xylanase; improve; thermophilicity; alkalophilicity; thermoclolerance; bleach; wood pulp; processing; wheat; maize; digestibilitiy-improving animal feed additive; starch production;
                                                                                                                                                                                                                                                                                                                                                        DNA sequence of the specification.
                                                                                                                                                                                                     AAV36098 standard; DNA; 573 BP.
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                  WPI; 1998-161100/15.
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AAV36098/c
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XyTv-101 (AAA48229), xyTv-102 (AAA48231), xyTv-103 (AAA48231), xyTv-2

(AAA48239), xyTv-110 (AAA48231), xyTv-110 (AAA48231), xyTv-2

(AAA48239), xyTv-7 (AAA48240), xyTv-4 (AAA48241), xyTv-5 (AAA48231), xyTv-7

(AAA48231), xyTv-7 (AAA48240), xyTv-4 (AAA48241), xyTv-5 (AAA48231), xyTv-3 (AAA
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                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermostable xylanases useful for preparing animal feeds especially poultry or swine feed, exhibits optimal activity under physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylanase; animal feed; digestion efficiency; thermostable;
feed pelleting; enzyme; XyTv-101, XyTv-102; TrX-103; XyTv-104;
XyTv-105; XyTv-106; XyTv-107; TrX-108; XyTv-109; XyTv-110; TrX-1;
XyTv-2; TrX-3; TrX-6; TrX-8; XyTv-4; XyTv-5; XyTv-7; Xyn A; Xyn B;
                           0;
                           Indels
                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                              T. reesei xylanase, XyTv-104, oligonucleotide.
                           Mismatches
     85;
     Pred. No.
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93.88;
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                           15; Conservative
                                                                           2 catcaaagtgattcgc 17
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  Best Local Similarity
Matches 15; Conserv
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Sung WL, Yaguchi M;

97EP-0115412 9605-0709912

(first entry)

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                                                                                                                                                                    The present sequence appears in the specification, which describes a method for modifying a Family II xylanase to improve its thermophilicity, atkalophilicity and or thermotolerance. This method comprises modification of amino acids 10, 27 or 29 of Trichoderma recess; xylanase
                                                                                                                                                                                                                                                                                                                  If or corresponding displaced amono words of another Family II xylanase, replacement of one or more union and sequences in the N-terminal region with corresponding aligned acqueres from another Family II xylanase to form a chimcoric xylanase and/on upstream extension of the N-terminable addition of upto 10 amino acids. The modified xylanases are useful for improving the bleechability of wood pulp by treatment at 55-75 degrees celsins and pH 7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-improving animal feed additives. They might also be useful
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels 0:
Modified xylanase enzymes - useful for improving wood pulp
bleaching, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the processing of wheat or maize for starch production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 573 HP; 163 A; 127 C; 136 G; 147 T; 0 other;
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Job time: 9216 sec
                                                                                                           Disclosure; Page 50; 84pp; English
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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Gaps

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Length 69; Indels

80.0%; Score 14.4; DB 21; 93.8%; Pred. No. 1e+02; iive 0; Mismatches 1;

Conservative

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Query Match

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AR096733 Sequence
AR147694 Sequence
AR147694 Sequence
U35021 Mycobacteri
U35017 Mycobacteri
U35017 Mycobacteri
B6264 Sequence 18
R6264 Sequence 18
R6264 Sequence 18
R6269 Mycobacteri
Z9586 Mycobacteri
Z9580 Mycobacteri
Z9530 Mycobacteri
Z9586 Mycobacteri
Z951313 Wibrio ch
Z806131 Neisseria m
ZF20613 Neisseria m
ZF20613 Neisseria g
ZF2061 N
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                                  AR096715 Sequence
AR147696 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA molecule encoding for cellular uptake of mycobacterium tuberculosis and uses thereof
Patent: US 6008201-A 5 28-DEC-1999;
Location/Qualifiers
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Sequence 5 trom patent US 6008201.
AR096715 GI:10025753
                                       AR096715

AR147696

AR147696

AR1476913

AR1476913

AR066212

AF06621

AF06621

AF06621

AF07028

MTCY2336

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AF1208061

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             DB
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1 (bases 1 to 650)
Riley, L.W.
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AR096715/c
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                                                                                                                                                                                                                                                                                       2944280
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                         1472140 seqs, 8248589755 residues
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Maximum Match 100%
Listing first 45 summaries
                                                               nucleic - nucleic search, using sw model
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em_htgo_lnu: *
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em_htg_hum: *
em_htg_lnu: *
em_htg_lnu: *
em_htg_loi: *
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Maximum DB seq length: 2000000000
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GenEmbl:*

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Database

Post-processing:

Title: Perfect score:

Run on: ŏ

Sequence:

Scoring table:

Searched:

08-AUG-2001

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Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K. Direct Submission
Submitted (29-And-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium: Mycobacterium tuberculosis complex.

Mycobacterium: Mycobacterium tuberculosis complex.

Mahairas, G. G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K.

Molecular analysis of qenetic differences between Mycobacterium boxis BGG and virulent M. boxis

J. Bacteriol. 178 (5), 1274-1282 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="site of deletion breakpoint in this organism. virulent M. bovis has additional 10 kbp at this site" 637~\rm c 416~\rm g 214~\rm t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBU35021 1604 bp DNA BCT 27-APR-1996
Mycobacterium bovis BCG DNA flanking deletion region 3.
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Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                        Unclassified.

1 (bases 1 to 1535)

Riley.L.W. and Chong, P.
DNA molecule fraqments encoding for cellular uptake of Mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 1 (01-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 18; DB 1; Length 1604; ilarity 100.0%; Pred. No. 40; Conservative 0; Mismatches 0; Indels 0
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red. No. 40;
Mismatches 0; Indels
                              PAT
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/sub_species-"BCG"
/db_xref="taxon:1765"
1400
                       AR147694 1535 bp DNA
Sequence 1 from patent US 6224881.
AR147694
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Matches 18; Conservative
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                                                                                                                                                                                               AK14/696 650 bp DNA
Sequence 5 from patent US 6224881.
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Sequence 1 from patent US 6008201.
AR096713
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Riley, L.W. and Chong, P.
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Riley, L.W.
                                                                                                                  189 CATGCCGTCGTATTGCTG 172
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Best Local Similarity 100.
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ADVEDAIRLYQGOTTDAELYSQLVARESBAVHFRAAESHVDNALDNFPFLHTNVIGTF
TILEAVRHGVRLHISTDEVYGDIELDDBARFTBESTPYNTSSPYSAFKAGADMLVRA
WYRRICVRATISNCSNYGPYQHVEKFIPRQITNCLTGLLKLXGDGGNVRDWIHVDDH
NSAVRILDRGRIGETYLISSEGERDNLTVLRSLLRLMDRUPDDFDHYTDRVAHDLRY
AIDPSRLYDELCWAPKHTDFERALRTTIDWYRDNESWLASLKHAGGRYQDAGQ"
1136. 1747
/gene="mnlc"
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/protein_id="Abb66648"."
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/db_xref="G1:2326979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhamnose biosynthetic genes related to a novel repeated sequence of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
705-035, South Korea
3 (bases 1 to 3453)
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Daemyungdong, Namku, Taegu
                                              Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds. U43540
                                14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                705-035, South Korea Sequence update by submitter on Aug 14, 1997 this sequence version replaced gi:1304703. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaccae; Mycobacterium; Mycobacterium tuberculosis complex.
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/protein_id="AAB66647.1"
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/organism="Mycobacterium tuberculosis"//db.xref="taxon:1773"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p1516"//clone="p151
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Submitted (14-AUG-1997) Tae-Yoon Lee,
Medicine, Yeungnam University, 317-1,
                                     DNA
                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis. Mycobacterium tuberculosis
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8 t 2 others
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Muhatras.G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K
Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology,
PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA
Loration/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 1; Length 3453;
Pred. No. 35;
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Mycobarterium bovis deletion region 3, 5' end.
U35017
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/note="previously known as rfbC"
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Mismatches
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misc_difference replace(1400. .>9281,"")
/noLe="absent in related
COUNT 1706 a 3191 c 2929 g 1453
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Mycobacterium bovis
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Matches 18; Conservative
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RESULT

TITLE

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/ Froder - "Care Lion - Fransporting AtPase, E1-E2 Tamily"
/ proder - "Care Lion - Fransporting AtPase, E1-E2 Tamily"
/ protein_id-"AAK44324.1"
/ (Protein_id-"AAK44324.1"
/ (Canslation="MYTYVECHHASVORIOLRISGMSCSACAHRVESTLNKIJCVKA
/ (Translation="MYTYVECHYNYMANDSALLEU-VTWAMPHENANDHAKULLIKL
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ANNEGTRVATIDTSEAVDAAALSETREWSGTWOALGSBAIYFEVANGVILIKL
ANSWELLISVGTRAATINSTYTVECHHSPIERSGTWOALGSBAIYFEVANGVILVEVL
ANSWELLISVGTRAATINSTYTVECHHSPIERSGTWOALGSBAIYFEVANGVILVEVL
ANGREANGGAAACANDMSANTGEARETRANGTOTALLGGUNIANSAAL
AGWYRLVOAQAQAKADAQRLABARETSSYFVPANLYJAALTAAGWLIAGGODDRAYSAAL
AVLVIACPCALGLATPTAMWASGRGAQLGIFLKGYKSLEATRAAGTILTTG
GRIQVSAYTAAPGWEADQVLALAATYVEAASHKASELGETAVFVEVDGFPCGVINAND
AVSGTYSGRAVVRQRSWIGSSSCHPUMRAARHAESLGETAVFVEVDGFPCGVINAND
AVNGSARAALADRGCHTMLTTORDESAAAVATRVGIDEVIADILLEGKVUVILEÜ
LKUKGHVVAMVGDGINDGPALARADLGMAIGRGTDMAIGAADILLEGKVUVILEÜ
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/codon_start-1
/rotable-11
/product="bypotherical protein"
/protein_id="AAK4432.1"
/db_xref="Ci:13879146"
/rotable-11
/db_xref="Ci:13879146"
/rotable-11
/rotable-11
/rotable-12
/rotable-12
/rotable-13
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VUIAAAGMGKVNTGI.TATLI.ADRFGCRTIVFTGVAGGLDPELC. IGDIVIADKVVQIIDF

GILTDERI, IRPYQHGII IPF I EIPTERLGY PVDPAVIDRYKHRIJGEPTI.API.STAAGGGGR

GHATYGCTI.TGDQYIAICERTRINELHEIJGGMAVEMEGGAVAQICASFDIIWI.VIRALI.

SHILAGADSGVDFNREVGHYAASSARVLIJELIATILAVITAG"

5105.../390
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vww:lrcgdfaiggpgrgapedaplimrgkalrqaiiiralgyerijkalylalaaw
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ayaviqavegyglwilkirws:yfavyatsifelelevholiakgitttryvtfyinvaav
vyilitskrifgyrggkrayiiverrgeolldleraamlt"
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/product.="5-methylthioadenosine
nucleosidase/8-adenosylhomocysteine nucleosidase,
                                                                                                                                                                                                                                     /note-"identified by Glimmer2; putative"
PPQTLHELRSHVRALLPGACIRRLLYGRVLVTWRAPV"
                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
/protein_id-"AAK44321.1"
/db_xref-"GI:13879145"
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/transl_table-11
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3791. .4162
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5105. 7390
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4206. .4973
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                                                                              /gene="MT0099"
3002. 3772
                                                                                                                                                                               /gene="MT0099"
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ELDGSGTVRGNIKVPAKLVVGSKFSTKMKLFGLPYRITSRVTALKPNELVECSHPLGH
RWRWEFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
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PYYTAVDIOAPVLRRAQTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /22. .1414
/gene="MT0095"
/note="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact; similar to SP:P16431 GB:X17506
PID:41684 PID:882614 GB:U00096; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
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(bases 1 to 9764)

(bases 1 to 9764)

Fleischmen, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Relonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Colonay, J.F., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
                                                                                                      BCT 27-APR-2001
section 7 of 280 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .9764 Mycobacterium tuberculosis CDC1551"
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/protein_id="AAK44320.1"
/db_xref="G1:13879144"
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/protein_id="AAK44319.1"
                                                                                                                                                            CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
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/db_xref="taxon:83331"
/note="clinical strain"
122. .1414
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Gill, J., Mikula, A. and Bishal, W.
Direct Submission
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1449. .2123
/gene="MT0096"
1449. .2123
                                                                                                                                                            Mycobacterium tuberculosis
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/gene="MT0096"
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/gene="MT0098"
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/gene="MT0098"
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                                                                                                                9764 bp
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Unpublished
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AE006921 AE000516
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/db_xref="61:2791846"
/translation="MKAATOARIDDSPLAMLDAVQRQRHEAGLKRCLRPRPAVATELD
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GLIFSSGYTANLGAVVGLSGPGSLLVSDARSHASLVDACRLSRAKVVYTPHRIVDAVD
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LIYELGIAGAPDVVMTTFLSKALGSGIĞVVLGPTPVRAHLIDAARPE I FDTGLAPAAV
GAARAALRVLAAEPWRPQAVLNHAGELARMCGVAAVPDSAMVSV I LAEPESAVAAAA
CLAAGVKVGGFRPPTVPAGTSRLKLTARASLNAGELELARRVLTIVLAVAKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zprotein, id. "Aday6956.1"
Zdb.,xr.-t. "G1.2791845"
Zh ans tai "na.2791845"
Zh ans tai ion. "Maata'ali/Pegi LavigahlahpysSickeavspvvavaalisa
witti Rolagi EvilandssaratalibiiGhpalajojakaratajojakoshibiidiibiidia
tartivotti paalotye esi sassvevaaraalajojakaratajojakaratajojaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /TransTallon="mkksmksgspalglammapmyaapglaaanpalkpynygoltdd
VVTARGLSQRDVPFSWAGGGTSGPTRGTGTGTNTVGFDASGLTQYAYAGATLKLPRSS
GOMYRVGORVLPQQARKGDLTPYGPEGTQSVALYLGKGQMLEVTDVGVSPVRTRGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ii.anslation."micsgvnppvaaameiegnaatprpipvtvaktsaigehaab
pngpedigpdagtesksaldepdektppruttriapwdvvctvvilavflavytukts
wiski.paftdnvcppdagtij.ypfGvnyyiypywmgGigaalatavicifysmi.kGwym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLI GGBARTELLELAAGULAGUDTAKALPAVTDVRVCGALGVITT 'DREVDUAVALPAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYTVOFSGPSIKPSNIKKRSSGRRSSKRPSSKRPSKGARPTGAGITIGAGIASARPASAR
PAASLKHRALTHTVPTAFSTFPKPASCFPLLSARSRRLVWVN"
                   Direct Submission
Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
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/product "putalive
adenosylmethionine-8 amino-7-oxononanoate
aminotiansperase"
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/note-"BioP; similar to MYCY336.34c"
/codon start 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"BioA; simitar to MrY336.35c"
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/note="ORE2; similar to MYCY336.36"
/codon_start-1
                                                                                                                                                                                                                                                                                 /hofe-"ORF1; similar to MrcY336.37"
/codon start l
                                                                                                                                                      /organism "Mycobacterium bovis BCG"
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                                                                                                                                                                                                                                                                                                                                      /transl_table 11
/product-"unknown"
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                                                                                                                                                                                                                                    /db_xret-"laxon: 43892"
                                                                                                                                                                                                                                                                complement (259, .1048)
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                                                                                                    Location/Qualitiers
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                                                                                                                                                                            /strain."Pasteur"
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/qene "biok"
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Arene "bioA"
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/qene-"biob"
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/qene="bioA"
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Yu,S.
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AUTHORS
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                                                                                                       FEATURES
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                                                                                                                                                            /product="hypothetical protein"
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DGMDCBVAREALSSAELDGERAPVFSARVDEHLGEGCSACKAWFTQVASQAGDLRRLAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFEAVLAKLAAPGATNPDDDHTPV TDTTPDAALDRDTKSQAOKNHOGILAGGRAALTAS
GKLGOHNGLPVSTYTTTLTDLQTGACKGFTCGGTLLI-WADV FRHTSHAHHYSPASGR
YPQATFDHGTPLALYHTKRLASPAQKIMLFANDRGCTKPGCDAPAYHSOAHHVTAWTS
TGRTDTTELTLACGPDNKLAEKGWTTFKNTHGHTEWLPPPHLDHGDFRTNTFHHPERF
                                                                                                                                                                                                                                                                                      RPVVPPVGRLG FRRAPRROHSPMTWRKWALLCVGIAO I ALGTVÕGFGLJVGFTHQHPT
GAGTHLLNESTSWSIALGVI MVGAALWPSAAAGLAGVI.TAFVA I LTGTVI VIDALSGAV
STTRI LTHLEVVI GAVLA I MVWRSASGPRPRPDAVAAEPD I VIJPDNASKGRRKGHLMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"conserved hypothetical protein"
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Mycobacterium; Mycobacterium tuberculosis complex.

[ (bases 1 to 10019)
] Yu, S. and Jacobs, W.R. Jr.

Cloning, sequencing, and identification of Mycobacterium bovis BCG biotin biosynthetic genes by complementing two Mycobacterium smegmatis biotin mutants
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                                                                                   /note="identified by Glimmer2; putative"
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/gene~?Mf0104"
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                                 complement(7337. .8185)
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                                                             /gene="MT0102"
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NFTAPPHLGLLGLLSVLAVVASALMWQWREHRGPQWVAGLSIGITTAAAIAAGVAALIAV
RLXGGALDFDTVPLSKGDHALTYTVTQAPPVFPARRPLQIALTLMWPAGIASIAYALLA
AGTRADULGGYPAVDPSSNARTEALEPQAPVS"
complement(9571: >10019)
/rock="ORF"|; similar to MTCY336.12"
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//ransl_table=11
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/kpl.fdhikvrttwptr.fpnpmtyragmarkavlaakvl.fgrkLskrpl."
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1 (bases 1 to 12412)
Stover, C. Kendall and Mahairas, G.G.
Stover, C. Kendall and Mahairas, G.G.
Virulence-altenuating genetic deletions deleted from myrobacterium
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Mycobacterium tuberculosis CDC1551, section 114 of 280 of the
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteriaces; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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Pred. NO. 27;
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vldlpddreeellalahevrmrwcgpeveveg11SlktrgcpedchercsosGlfaspv
vrawldipsyveaarqtascattecttaavrgoperlaaqvaagteairneveinia
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CLVRRLDAVGHTLINOLDTOASEEELGGTLCCALANRLRITKPDAALH TADAADLGPR
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/note="ORF10; similar to MTCY336.13c"
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/note="ORFG; similar to MTCY336.32c"
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/transl_table=11
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/note="ORF7; similar to MTCY251.13c"
/codon_start=1
                                                                                    /note="BioD; similar to MTCY336.33c"
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/note="ORFB; similar to MTCY336.16"
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/protein_id="AAB96962.1"
/db_xref="G1:2791851"
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/gene="bioB"
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gene

CDS

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EMANSYPIDHEHRAMASEN FROTIVOLDGI HABADINSHVOLISPATY UGLIMAY SGGGL
ASAMAARAY TITALAH I SANGSINYGIJAJITERRI NOTTIJAGLEALIVVAALQHISY
GLARVI REHANINGIQI I LIQUTERIT VDAV FRINGRUNGDELDGPLEDI LSTPEVSHV
FIDITILISAAVETITALI VOAVHDYLIDVSDI IDALADSSYTAGGANVITYHRDI ESEHVSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5660. .6193)
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SRSI SSRRAGPLRPAGHGLATPKKRPHKHRTKPQTRHIPEQPA I KKHVTAKMI,PDPPS
AGHL"
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Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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complement(104. 826)
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complement(831. .1499)
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Unpublished
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score is 0.930"
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Direct Submission
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Pred. No. 26;
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7468. .9051
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100.0%;
                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                  7468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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VERSION
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                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
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FOCUS

δŏ qq

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IDGYKEFPGEWALVPVGATMLMILAGANROGHPGTRDRLPLPNRLLATAPI.VALGAMA YSWYLMHWPLLIFWLSYTGHRHANFYEGAVULVGCLLAVITTRLVEDBLYFYAPAGV SRSPAAVPPI.PURRLERFRYT IVLGSVYALLGVALLATSFTWREIIVIVORAAGKEL.SGLS RIDYPGARAI. IDVRYPKLLKRRPTVLEVRHDLPTSTROGGISDFVNIAI I NCTYGDVD APRTTALAGGSHAEHWLTALDLLGRMHHFKVVTYLKMGCPLSTEEVPI.IMGNNAPYPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVAVFHVWFGRVSGVDVFLALSGFFFGGKILRAALMPDLSLSFIAEV TKL FRKLLPA
LVVVLAGCALLT1APPOGTRREAFANOSLASIGYYQNWELASTVSNYI.RAGEAVSPLQ
HIWSMSVQGQFYLAFLLLVAGCAYLLRRLFRGPRAPYLRTMFVVLLSTLTLASFIYA1
VAHHAYQATAYYNTFARAWELLAGALVGAVVBHVRWPWMLRTAVATAALAA1I.SCGAL
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/translation-"MLTLSPPRPPALTPEPALPPVTMGTRTTGFVHHDLDGLKGVAIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Relibbe, (MICY336.48), len: 729. Unknown membrane protein, some similarity to 005402 HYPOTHEFICAL 72.2 KD PROTEIN from B. subilits (64 as) opt: 384 E(): 4.8e-17; 29.1% identity in SYR aa overlap and to hypothetical protein in Hindluenzae. N terminal half hydrophobic. FASTA results, 29.3% identity in 247 aa overlap. Thearse
                                                                                                                                                                                                                                                              Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium Liberchiosis Sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genelique Moleculaire Bacterienne, Institut pasteur, 28 rue du Dorteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:2117243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of M. Luberchlosis sequencing at the Sanger Centre are available on the World Wide Web.

(UKL, http://www.sanger.ac.uk/Projects/M_tuberchlosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers gene prediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observod/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon date, quy, or tup, which is preceded by an upstream ribusome binding site sequence (optimulty 5-13pp before the initiation codon). If this cannot be identified we choose the most upstream
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
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/strain="H37Rv"
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/protein_id-"CARU9072.1"
/db_xref-"G1:2117272"
                                                  complete genome sequence
Nature. 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xret-"taxon:83342"
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/clone-"Y48"
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/note: "re-"
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/qene-"kv1565c"
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gene

CDS

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3791. :5104
//gene="bloA"
3791. :5104
//gene="bloA"
//geness class-ling pyridoxal-phusphate altachment annortansferase class-ling pyridoxal-phusphate altachment site (ps00600). PsNPATesults, BloA_MYCLE p4548 (436 aa)
//gene="bloA"
//gene="b
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LAKLLVDITPAGLDTVFFSDSGSVSVEVAAKMALQYWRGRGLPGKRRLMTWRGGYHGD
TFLAMSICDBHGGMHSLWTDVLAAQYRAPQVRRDYDAYSAAREAQLAQHAGELAAVV
EPLAGGGGGGRFHDPRYTHDLRDICRYEVLLIFDTDTGFGRTGALFAADHAGVSP
DIMCVGRALTGGYLSLAATLCTADVAHTISAGAAGALMHGPPFMANPLACAVSVASVE
LLLGQDWRTRITELAAGLTARGLDTARALPAVTDVRVCGAIGVIECDRPVDLAVATPAA
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/translation="MVTMTSWPSRLFAFTDNVCPPDACPI,VPFGVNYYIYPVMWGGIG
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/translation="MAAATGGLTPEQIIAVDGAHLWHPYSSIGREAVSPVVAVAAHGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOWVOAAMAKLVADHPDYVETTSTREWNIKPGDVMPATYVGIWQTFADNNIPVLAMR
DTPWLVKDGQPFIPADCLAKGGNPQSCGIARSKVLVDRNPTLDFVARFPLLKPLDMSD
ACRTPOTCRAVGGNVLVYRDSHHLTPTYMRTWTSELGRQIAANTDWW"
COMplement (2327 3019)
                                                                                                                                                                                                                                                                                                                                                  Jote- *RV156C, (MTCY336.37), len: 230. Function: unknown probably exported has QQAPV repeats at C-terminus, similar to hypothetical M. leprae protein, to putative invasins 1.2(007390, 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_LISMO P217171. FASTA results, Q49634 COSMID B1170 (246aa) opt: 957 E(): 0, 70.0% identity in 207 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3259. .3543)
/gene="Rv1567c"
/note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse
score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="possible RBS, AAGGAGG, for Rv1566c" complement(3258. 3263) /note="ASNI site: ATTAAT; probably linking fragments
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4541. .4654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein Rv1566c"
/protein_id="CaB09071.1"
/db_xref="G1:2117271"
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/product="hypothetical protein Rv1567c"
/protein_id="CAB09070.1"
/db_xreff="G1:2117270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overlap. TBparse scoreis 0.890"
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/db_xref="G1:2117269"
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                                                                                                                                                                                                                                                      complement(2327. .3019)
/gene="Rv1566c"
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/transl_table=11
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AALKSRIDEQKAVVVTDSVFSADGSTAPVRELLEVCKRIGALTLIVDEAHGLGVKRIGGRG
LLYFLGLAGAPDVVMTPTLSKALGSQGGVVLGPTPVKAHLTDAARPETEDYGLAPAAV
GAARAALKVLQAEPWRPQAVLNHAGELARMCGVAAVPDSAMVSVTLGEPESAVAAAAA
CLLAGVKVGGFRPPTVPAGTSRLRLTARASLNAGELELARRVLTDVLAVAKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Lrānslation-"MKAATQARIDDSPLAWLDAVQRQRHEAGLRRCLRPRPAVATELD
LASNDYLGLSRHPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQQFEABLAFFVGAAA
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Mycobacterian: Mycobacterianum tuberculosis complex.

1 (bases 1 to 38380)

Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Elgimeier,K., Gas,S., Barry III,C.E.,
Tekaia,F., Badcock,K., Hasham,D., Rrown,D., Chillingworth,T.,
Connor,R., Davies,R., Hovlin,K., Feltwell,T., Gentles,S.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., McLean,J.,
Squares,S., Sqares,R., Suiston,J.E., Taylor,K., Whitchead,S. and
Barrell,B.G.
                                                                                                                                                      probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-11 pyridoxal-phosphate attachment site (PS00599). FASTA results, B HOP-MYCLE P45487(385 aa) opt. 1971; E(): 0; 80.18 identity in 381 aa overlap. Also similar to MTCY10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in 393 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H7Rv complete genome; sequent 5/162.
                                                                                                                                     (MTCY336.34c), bioF, len: 386. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note="PS00600 Aminotransferases class-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="pS00599 Aminotransferases class-II
pyridoxal-phosphate attachment site"
6258. .6938
6258. .6938
6258. .6938
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                        pyridoxal-phosphate attachment site"
5101. .6261
/qene="biof"
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                                                                                                                                                                                                                                                                                                                                                                                            /protein_id-"САНО9068.1"
/db_xref="G1:2117268"
/db_xref="SWISS-PROT:006621"
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Nature. 393 (6685), 537-544 (1998)
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Mycobacterium tuberculosis H37Rv
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
/product~"bioF"
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                                                                                                                                            /note="Rv1569,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 17614 CARGCGTGGTATTGCTG 17631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5806. .5835
/gene~"bioF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98295987
2 (bases 1 to 38380)
Parkhill,J.
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                                                                                                                 /gene="biof"
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VERSION
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Auches "KVOU87, (MTVY251.05), oxidoreductase, len: 492, hyek, similar to HYCE_ECOLI P16631 formate hydrogenlyase subunit 5 (569 aa) FASTA scores, opt: 680, z. score: 4804. E(): 1.8e-38, (31.28 identity in 449 aa overlap) and to NU0D_ECOLI P33600 nadh dehydrogenase i clain d, (407 aa) FASTA scores.opt: 245, z. score: 293.1, E(): 8.9e-10, (24.5% identity in 368aa overlap)" // runsl_table_11 // runsl_table_1
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/translation="MSVYKIIAPSRYRLRQTRSTVKGRSGSLSWRRVFTGDLG1AVWG
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FLDGSGTVHGNTRVPRALVVGTRSTVRMKLFGLPVRTTSRVTALKPHSHIPLGH
RWRWPFFSI,SFTLTHVTFTFDYHAAGAIKNGLKFYEMTGFAKSNAAG1FATLAKI.SDQ
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EDALGI TELEBEVIRI LKALL VELERT, YHRADIGALANDVÖYSLANAHAĞBI UKBULLIKR
NAAVTGHELLEKTALRAGVALRALEPIYDELAALAVDI AEVATLI TLANSVV DIFFAGTA
VLHPIDASALGCLGVARKASÜLKSINAKVEHPT IVLE PIELGALIVÜLVLARYT VEKÜEF
AASAALAQH LVESHYGET EY AATLIHPVGAPSSGIG I VEGWEGT LVHKVELLIVÜCKLTTR
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VV LGSVGTAVAFLGTVILLY FAARDSGAAAGALNED I LAEHAAGLDFGVARLAGGLLL
LGYGAKAGLEPEHTWLADAHSQAPAFVSALMSGVCLLAVAFSVL I RELEFTLLAVSGPAY
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AMFASELA I AKSLANEKLAWV LGAALILITA I GFTALARNSGKMI JASTVAAGALATI TVP
ATAAAAI MVG I VVSAALAT TAGPLAD LI GTAASNVGLP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transtation="witchlinalidaphaastashattowrrthalsattviacav
ampewiiggageglachlikabalfvvmlvvtglvchlataastcytherlahenfdr
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MLDNGIAATAFLLTAGVPL[VELGASLDVLFAVIVIGVLTGKLRR1FGDADLDKLREL
                                                                                                                                                                                                                                                                                                              /hote="RV0086, (MTCY251.04), oxidoreductase, len: 488, hyco, most similar to spiP77437 HYFF_ECOLI HYDROGERASE-4 COMPONENT F(EC 1.~ (526 ad.), FASTA scores: opt: 948 x-score: 1177.4 E(): 0; 35.9% identity in 493 ad overlap. Also similarlo E. coli d9087711 & NUOL_ECOLI F33607 hadh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         delydrogensed chain 1 (613 and FASTM scores 354.9 (F): 1.2e-13, (27.9% identity in 488 ad overlap), and to Nich ECOLI P33608, nach delydrogense i chain n (425 ad), FASTM scores, opt. 375, z-score: 471.4, (E): 3.9e-14, (25.0% identity in 432 ad overlap)" //codon_start=1 //thus=[Lable=1] //thus=[
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/product-"hypothetical protein Rv0088"
/protein_id-"CAA98924.1"
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/note-"RV0088,
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/qене-"hyeE"
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1629. .3095
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VASTIDHPRIVVSLAĞVLANINYALIALIVDNMATHILLI-TIMVIHSAMVLEYAG
PREALVEMAAGMRITYALLALLANIFLPWGIAGAAPTALIOVLTGVVAVAAKVAILAVILA
ATFEVFLAKLRIFRVPELIAGSFLLALLANIFAVAANFFTVGA"
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AAIPLLRGIRDNDRALIAVGLAVLALRALVLPWLLARAVGAEAAAQKEAFPLVNTASS
LLITAGLTLTAFAITQPVVNLEPGVTINAVPAAFAVVLLALFVMTTKLHAVSQAAGFL
                                                                                                                  tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge Callo 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
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DLLKQLGRQQITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPIDPSADLFAVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markow Model of TW genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position 6 + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (Higy 4fg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv0085, (MTCY251.03), len: 220, hycv, similar to
splP77524 HYFE_ECOLI HYROGGENASE-4 COMPONENT E: (216
aa), FASTA scores: opt: 204 z score: 272.1 E():1.2e-07;
25.58 identity in 216 aa overlap"
           Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                               in Jun 27, 1998 this sequence version replaced gi:1405752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mycobacterium tuberculosis H37kv"
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/protein_id="CAA98920.1"
/db_xref="GI:1405754"
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/db_xref="GI:1405755"
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/db_xref="taxon:83332"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="H37Rv
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6, ass
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967. 1620
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/gene="hycP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .35889
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           T LTLE
JOURNAL
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probable precured of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 053863 SERINBFORTHSES (390 aa) opt: 241; E(): 8e-07; (38.0% identity in387 aa overlap), similar to MTCX15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAALIJTTAKEE YETTRI SCALAASC ITAGGGLMIJVRNALGTNYTRY SDATAGVVAAA
GLAALIJTAV LA YETYREE LASTAS TAT IFGAVAGLLAVENYGVIISVLVAMBAAA
FSVLAMK ITGTG TELTAVA TAVVYAATI VGGTITAAVETGSLATLASTALLEVS
ARAVILLAGLSEHLPPALIPODADALITTERANKADAMITSLLAAFAASATIGA
IGTAVATHG HRSSROG IALAAVGALLLARARSADYHKSLVETIGG TTVATPETVA
ADRALEHGEWIAALTAMLAAVAMFLGFVAPALSLSPVTYRTIELLECLALIAMVETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mptship::lrrvtvHaGaQaVDLTLPAAVPvATLLPSTVD1LGDR
GaSPATAARYOLSALGAPALPMATTLAQCGTRDGAVLVLHKSSAQPPTPRCDDVAEAV
                                                                                                                                                                                                                    of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct
                                                                                                  been renumbered from the original cosmid submissions but the old
gene designations are in brackets after the new gene numbers.
Gene prediction was based on a Hidden Markov Model of TB genes
implemented in TBparse (Krogh) supplemented with visual inspection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Rv3448, (MTCY77.20), len: 467 aa. Unknown membrane
                                                                                                                                                                                                                                                                                                     initiation codon. Where possible we choose an initiation codon (alg. qtg. or ttq) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). It this cannot be identified we choose the most upstream
                                         available on the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport systems inner membrane comp signature. Some similarity to ALG21940[MTV035_18 Mycobacterium tuberculosis (472 aa) fasta score, opt: 429 z-score: 480-4 E(): 1.1e-19; 28.2% identity in 479 aa overlap" //transl_tahle-11
//transl_tahle-11
//protein_in_publiciteal protein Rv3448"
//db_xref="G1:3261767"
                 of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein, contains PS00402 Binding-protein-dependent
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/note-"PS00402 Binding-protein-dependent transport
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    43401
    /orqanism-"Mycobacterium tuberculosis H37kv"
    /strain-"H37kv"

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/strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref-"taxon:83332"
/clone="Y77"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/qene="Rv3449"
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/gene="Rv3449"
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78. .164
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initiation codon.
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Actinomycetales; Corynebacterineae; Mycobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (Dases 1 to 43401)
Cole,S.T., Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry Ill,C.E.,
Takia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
Connor,R., Davies,R., Davlin,K., Feltwell,T., Gentles,S.,
Hamilin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandream,M.A., Rogers J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
NL Nature. 333 (6885), 537-544 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDQPMNANTHYDALL;DAWVPLGTQCVLDVGCGDGLLAARLARRI
PYVTAVDIDAPVLRRAQTRFANAPIRWLHADIMTAEL;PNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANKVKGKWEHSAPIKWP
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                                                     seyment 147/162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="aaggag, potential rbs upstream of Rv0090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 18; DB 1; Length 38380;
Pred. No. 22;
; Mismatches 0; Indels 0;
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295390 AL123456
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/product="hypothetical protein Rv0090"
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/product=hypothetical protein Rv0089"
/protein_id="CAA88925.1"
/db_xref="G1:1405759"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:010886"
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/gene="Rv0090"
                    'gene="Rv0089"
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Matches 18; Conservative
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MTY13E12/c
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REFERENCE
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/product="hypothetical protein Rv3450c"
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/db_xref="SPTREMBL:006316"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAALAYAVDVKNAVIVAAAGNTGGAAQCPPQAPGVTRDSVTVAVSPAWYDDYVLTVGS
VNAQGEPSAFTLAGPWVDVAATGEAVTSLSPFGDGTVNRLGGQHGSIPISGTSYAAPV
VSGLAALIRARFPTLTARQVWQRIESTAHHPPAGWDPLVGNGTVDALAAVSSDSIPQA
GTATSDPAPVAVPVFRRSTPGPSDRRALHTAFAGAAICLLALMATLATASRRLRPGRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown but similar to Rv3895c MrCY15F10.17 (FASTA score: 1.6e-27; 36.48 identity in 475 aa overlap); possible membrane spanning region near N-terminus, and to Y14967|MLCB628_16 Mycobacterium leprae cosmid H628; (481 aa) opt: 708 z-score: 710.9 E(): 4.5e-32; 32.9% (MrV027.04)*
                                                                                                                                                                                                                                                                                                                                             PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGAGQRVAVIDTCVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQSSSKFAPVGDPSSTGVGDVDTMAKAVRTAADLGASVINISSIACVPAAAAPDDRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /, mote="PS00137 Serine proteases, subtilase family, histidine active site" // 1856. 2458. 2458. 42488 // 1858. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 4258. 42588. 4258. 4258. 4
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                                                                                                                                                                                                                                                                                                                                                                                                            RHRRLPKVVAGGDYVFTGDGTADCDAHGTLVAGIIAAAPDAQSDNFSGVAPDVTLISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPELSRANASVARDTVAPGP"

complement(1049. .4081)

//note="Rv3450c"
/note="Rv3450c"
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/gene="Rv3450c"
complement(2810 .4222)
/note="Rv3450c"
/note="Rv3450c" (MTCY13E12.03c), len: 470 Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4388. .5131
/gene="Rv3451"
/note="Rv3451, (MTCY13E12.04), len: 247. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PS00136 Serine proteases, subtilase family, aspartic acid active site"
1862. 1894
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/note="possible RBS, GGAG,
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/gene="Rv3451"
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/gene="Rv3449"
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/LTATSTATION=*MSTNPKPORKTKRNTNRRPQDVKFPGGGGIVGGYVLLPRKGPRL
GVRATRKTSERSQPRGRRQVIPKARHPEGRTWAQPGYPWPLYGNEGLGWAGWILSPRG
SRPSWGPTDPRRRSRNLGRVIDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLED
                                                                                                                                        /translation="MCAGALITAVVLLIALGAVWTPVAFADGCPDAFYTFARCTGEPP
GIGRYGOAFVDSLROOTGMFIGVTPVNYAASRLOLHGGDGANDAISHIKSMASSCPNT
GIGRYGOAFVDSLROOTGMFIGVTPVNYAASRLOLHGGDGANDAISHIKSMASSCPNT
GIGRYGOAFVDDIVAGCHGFIGVERSCHIDGYIPTYTTOAASFVVORLRAGSSVPH
LPGSVPQLPGSVLQMPGTAAPAPESLHGR"
LPGSVPQLPGSVLQMPGTAAPAPESLHGR"
/ Gene="Rv4451"
//note="PS00155"

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Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E2, p7, NS2, NS3, NS4a, NS4b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 9600)
Mokhonov, V.V., Samokhvalov, E.I., Novikov, D.V., Shatalov, A.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mokhonov, V.V., Samokhvatov, E.I., Novikov, D.V., Shatalov, A.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"kv3452, (WTCY13E12.05), len: 226. Function:
probable cutinuse precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (09-AUG-1999) Molecular Genetics, Ivanovsky Virology
Frants Gamaleva Str., 6, Moscow 123098, Russia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/note="isolated from acute hepatitis patient scrum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF176573 9600 bp RNA VRL 18-AUG-199
Hepatitis C virus polyprotein precursor, gene, complete cds.
AF176573. GI:5738246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 18; DB 1; Length 43401; 100.0%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
/product-"hypothetical protein Rv3451"
/protein_id="CAB08717.1"
/db_xref="C1:2104374"
/db_xref="Sw1SS-PROT:006318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5165. .5168
/note-"possible RBS, GAGG, for Rv3452"
5178. .5858
/qene-"Rv3452"
5178. .5858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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/protein_id="AAD50312.1"
/db_xref="GI:5738247"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Hepatitis C virus"
/strain-"274933KU"
/isolate-"lb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342. .9374
/note="cleaved into C, El,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS5a, and NS5b proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:11103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           institute, Gamaleya Str., 6,
Location/Qualifiers
1. .9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /qene~"Rv3452"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 9600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prilipov, A.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                        misc_feature
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LOCUS
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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AUTHORS
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SOURCE
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Query Match 91.1%; Score 16.4; DB 14; Length 9600; Best Local Similarity 94.4%; Pred. No. 2.16+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: April 2, 2002, 22:46:14 Job time: 12544 sec

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April 3, 2002, 08:04:13; Search time 165.4 Seconds (without alignments) 24.647 Million cell updates/sec
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11: /cgn2_6/ptodated2/ina/5A_COMB.seq:*
12: /cgn2_6/ptodated2/ina/5B_COMB.seq:*
13: /cgn2_6/ptodated2/ina/6B_COMB.seq:*
14: /cgn2_6/ptodated2/ina/fB_COMB.seq:*
15: /cgn2_6/ptodated2/ina/pcrucs_COMB.seq:*
16: /cgn2_6/ptodated2/ina/pcrucs_COMB.seq:*
17: /cgn2_6/ptodated2/ina/pcrucs_COMB.seq:*
18: /cgn2_6/ptodated2/ina/pcrucs_COMB.seq:*
18: /cgn2_6/ptodated2/ina/backfiles1.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                  351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM nucleic - nucleic search, using sw model
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18
                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 18, Appl		_`.	د _``	Sequence 18, Appl	Sequence 18, Appl	۹,	19,	7	m	Sequence 6, Appli	9	Sequence 1664, Ap	ထ်	Sequence 8, Appli	Sequence 7, Appli	Sequence 5, Appli	5,	Sequence 7, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli
ID	US-08-390-878-18	US-08-461-002-1	US-08-689-411-1	PCT - US94 - 09863 - 1	US-U9-103-840A-1 US-08-709-912-18	US-09-047-370-18	US-09-201-641-1	US-08-322-742-19	US-09-198-839-2	US-09-198-839-3	US-08-345-756-6	US-08-625-198-6	PCT-US96-05320A-1664	US-08-345-756-8	US-08-625-198-8		US-08-345-756-5	US-08-625-198-5	605-1	US-08-547-182-4	US-08-577-121-3	US-08-985-700-3	US-09-149-161-3	PCT-US95-16916-3	US-08-096-044C-2
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Score	18	16.4	16.4	16.4	16.4		14	13.8	13.8	13.8	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4			13.2		•	13.2
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Query Match 100.0\$; Score 18; DB 1; Length 12412; Best Local Similarity 100.0\$; Pred. No. 0.46; Matches 18; Conservative 0; Mismatches 0; Indels 0

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Sequence 9, Appli Sequence 1, Appli Sequence 11, Appli Sequence 15, Appli Sequence 29, Appli Sequence 15, Appli Sequence 15, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli	ENETIC DELETIONS and Crew Tower, 20th
US-08-096-044C-9 US-08-149-105-1 US-08-17-847-1 PCT-US91-01327-11 S248670-1 US-08-431-080-25 US-08-431-080-25 US-08-431-080-25 US-08-12-4-934A.5 US-08-12-4-934A.5 US-08-12-4-934A.5 US-08-12-4-934A.5 US-08-12-4-934A.5 US-08-103-840A-2 US-09-103-840A-2 US-09-103-840A-2 US-09-103-840A-2 US-09-103-840A-2 US-09-103-840A-2 US-09-103-840A-2 US-08-641-873-17 US-08-641-873-17 US-08-641-873-17 US-08-641-873-17	ALIGNMENTS R. R. Ty G. NOWINSEND Khourie Stendit Street
73.3 1112 3 773.3 1530 1 773.3 1530 1 773.3 1557 5 74.3 1882 1 74.4 1882 2 74.4 1882 2 74.4 1882 2 74.4 1882 2 74.4 1882 2 74.4 1882 2 74.4 440.765 4 74.4 440.765 4 74.4 440.765 4 74.4 440.765 4 74.4 440.765 4 74.4 440.765 4	ALIDIN T. 1 1-30-878-18 -30-878-18 coll No. 5700684 NERAL INPORMATION: APPLICANT: Stover, Charles K. APPLICANT: Stover, Charles K. APPLICANT: Stover, Charles K. APPLICANT: Mahairas, Gregory G. TITLE OF INVENTION: VIRULENCE-AFTEN NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend STREET: Floor CITY: San Francisco CUNNTRY: USA CUNNTRY: USA XIP: 94105 COMPUTER READABLE FORM: MEDIUM TYPE: Floopy disk COMPUTER READABLE FORM: MEDIUM TYPE: Patcut in Release #1.0. CUNRENT APPLICATION INTRESS APPLICATION NUMBER: US/08/90.878 FILLING BATE: 17 FEB 1995. ALPHING BATE: 17 FEB 1995. ALPHING BATE: No mandless: 19 5/1A 1 TELECOMMUNICATION INPORMATION: TELECOMMUNICATION INPORMATION INPORMATION INPORMATION INPORMATION
28 13.2 7 33.0 13.2 7 3.3 13.2 7 3.3 13.2 7 3.4 13.2 7 3.5 13.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7 3.2 7	RESULT 1
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                  APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Fleppy disk COMPUTER: HW PC COMPATIBLE OFFKATING SYSTEM: PC-INS/MS-10/8 SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08689411; Patent No. 6224881; GENERAL INFORMATION: APPLICANT: Riley M.D., Lee W. APPLICANT: Chong, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-689-411-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-1
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NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENCTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: double
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CLASSIFICATION: 536
                                                                                                       FILING DATE:
CLASSIFICATION: 435
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-689-411-1
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Sequence 1. Application US/08461002
Patent No. 6214543
GENERAL INCPRATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                           Sequence 1, Application US/08464052
Sequence 1, 6008201
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Updake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT . PLICATION DATA: APPLICATION NUMBER: US/08/464,052 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPRAKE (716) 263-1504
TELEPRAKE (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.4; DB 3;
Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester CTY: Rochester COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

CONPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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94.48;
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STRANDEDNESS: double
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STATE: New York
COUNTRY: U.S.A.
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Matches 17; Conserv
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US-08-461-002-1
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                                                                                                RESULT 2
US-08-464-052-1
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TITLE OF INVENTION: DNA MOLECULE FRACMENTS ENCODING FOR TITLE OF INVENTION: CHILULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Hox 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               91.1%; Score 16.4; DB 4;
nilarity 94.4%; Pred. No. 2.6;
Conservative 0; Mismatches 1;
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE,DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPAX: (716) 263-1304
TELEPAX: (716) 263-1500
INFORMATION FOR SEQ ID NO: 1.
SEQUENCE CHARACTER/STICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,727
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1504
TELEFAX: (716) 263-1500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
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CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ 1D NOS: 2 SEQ TWARE: Patentin Ver. 2.1 SEQ 1D NO 1 LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: //desc - "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: O LSCH M., MALLOCH F
RED ISHRAFI H. NUMBER: 27290
REFERENCE/LOCKET NUMBER: 1035,2000
TELECOMMUNICALION INFORMATION:
                                                                                                                      ; OCHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08709912; Patent No. 5759840; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      DD 1789446 ACGTCAAAGTGATTCGCG 1789429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INPORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
93.8%;
                                                                                                                                                                                                                           91.18;
94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 573 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.45
Matches 17; Couservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
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US-08-709-912-18
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-08-709-912-18/c
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                                                                                                                TYPE: DNA
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APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VERNER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 2.6;
0; Mismatches 1; Indels 0
                                          Score 16.4; DB 4; Length 1535;
Pred. No. 2.6;
                                                                                                                                                                                                                                            Sequence 1, Application PC/TUS9409863
GENERAL INFORMATION:
APPLICANT: Piley, Lee W
TITLE OF INVANTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMINICATION INFORMATION:
TELEPHONE: (716)263-1000
INFORMATION FOR SEQ 10 NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 Dass pairs
                                                                Pred. No. 2.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: -PCT/US94/09863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09103840A; Patent No. 6294328
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0
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nilarity 94.48;
Conservative (
                                              Query Match 91.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-09-103-840A-1/c
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PCT-US94-09863-1
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Matches
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Gaps
Length 4411529;
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sund Dr., Wind L.
APPLICANT: Yaque'li Dr., Makolo
APPLICANT: Yaque'li Dr., Makolo
APPLICANT: Yaque'li Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fitzpallic, Cella, Harper, and Scinto
STREET: 277 Park Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PY: Compatible
OPERATIC SYSTEM: PC-DOS/MS-INS
SOFTWARE: Patentin Keledse #1.0, Version #1.30
CHRENT APPLICATION DATA:
FILING DATE: 09 SEP 1996
CLASSIPHCALION: 445
     DB 4;
Score 16.4; DB pred. No. 7.8; 0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Cunningham Jr, Francis X
APPLICANT: DellaPenna, Dean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-322-742-19
                                                                                                                                                                            SEQ ID NO 1
LENGTH: 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                   FEATURE:
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          Gaps
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                                                                                                                                                                                                                 APPLICANT: Stand Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuchiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpartic, Cella, Harper, and Scinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWART: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: -US/09/047,370
          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.4; DB 2;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1039.2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09201641A; Patent No. 6232530
                                                                                                                                                               Sequence 18, Application US/09047370 Patent No. 5866408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: OLSEN MY, WARTEN E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2802
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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93.8%;
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 80.0
Best Local Similarity 93.8
Matches 15; Conservative
                                                               471 CATTAAAGTGATTCGC 456
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            Conservative
                                             2 catcaaagtgattcgc 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: pTvX(3-190)
US-09-047-370-18
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10172-0194
                                                                                                                                                                                                                                                                                                                                                                                                              New York
                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                 US-09-047-370-18/C
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US-09-201-641-1
            15;
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              Matches
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Gaps
TITLE OF INVENTION: Mariod for Regulating Carotenoid Biosynthesis in TITLE OF INVENTION: Marigolds
FILLE REFERENCE: Quest 41-162
CURRENT APPLICATION NUMBER: US/09/201,641A
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ 1D NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 4; Length 1959;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM FS/2 Model 50% or 558X OPERATING SYSTEM: IBM P.C. bus (Version 3.30) SOFTWARE: Wordsetect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/048003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
Z.P. 02110-2804
COMPUTER REALDABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: September 1, 1992
APPLICATION NUMBER: 07/844,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JMBER: 07/844,296
February 28, 1992
JMBER: 07/552,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/08322742 Patent No. 5688641 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: February 28, 1992
APPLICATION UNMERK: 07/552,216
FILING DATE: February 28, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     COTHER INFORMATION: beta-cyclase US-09-201-641-1
                                                                                                                                                                                                                                                                                                                                                                                                                    77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                      ORGANISM: Tagetes erecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 catraaaqtgatte 15
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DB 4;
                           Pred. No. 81;
0; Mismatches
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93.3%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33229/236/PIHI
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
          Score 13.8;
Pred. No. 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPPLICATION NUMBER: 05/08/345,756
FILING DATE: 22-NOV-1994
CLASSIFICATION: 800
ATORNEY AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
REPERNEK/POCKET NUMBER: 33229/236/1
TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08625198
Patent No. 5755324
GENERAL INFORMATION:
APPLICANT: BARECZYDSKI, Chris
APPLICANT: BALCOUT, Eric
APPLICANT: HALLOIL, Jiro
APPLICANT: Miki, Brian
                                                                                                                                                                                                                        Sequence 6, Application US/08345756; Patent No. 5633438; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         Baszczynski, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; repolacty; linear; kolaconic); Molacule PPPE; bNA (aparonic)
US-08-345-756-6
                                                                                                              2059 catcaaattgattcacq 2075
                                                                                         2 catcaaaqtqaftcgcq 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 34 base pairs
TYPE: meleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 catcaaaqtgattcy 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER RESDABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 CATCAAAGTGATGCG
          Query Match
Best Local Similarity
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: USA
20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-625-198-6
                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                            US-08-345-756-6
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APPLICANT: Kang, Angray S.

APPLICANT: Kang, Angray S.

TITLE OF INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MUDIFIED

TITLE OF INVENTION: FILAMENTOUS PHAGE
FILE REFERENCE: SCR2111S

CURRENT APPLICATION NUMBER: US/09/198,839

CURRENT FILING DATE: 1998-112-24

PRIOR APPLICATION NUMBER: PCT/US99/18207

PRIOR APPLICATION NUMBER: BCT/US99/18207

NUMBER: DATE: 1998-08-12

SECTION NUMBER: BCTONOS: 11

SOFTWARE: PATENTING DATE: 2.1
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kang, Angray S.
TITLE OF INVENTION:
TITLE OF INVENTION: FILAMENTOUS PHAGE
FILE REFERENCE: SCR2111S
CURRENT APPLICATION UNBER: US/09/198,839
CURRENT FILING DATE: 1999-08-11
PRIOR PILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
SOFTWARE: PALENCHIN NUMBER: OF 10/196,326
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2: 11
SEQ ID NO 2: 12
LENGTH: 2321
                                                                                                                  Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: pORFES IV
US-09-198-839-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: PORFES II
US-09-198-839-2
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                                                                                                                0;
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                                                                      DB 1; Length 358;
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                                                                        Score 13.8; DB
Pred. No. 61;
0; Mismatches
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Pred. No. 81;
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US-09-198-839-3
; Sequence 3, Application US/09198839
; Patent No. 6190908
                                                                                                                                                                                                                                                                                           Seguence 2, Application US/09198839 Patent No. 6190908
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TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.78;
88.28;
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88.28;
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                                                                                               Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
; TOPOLOGY: linear
US-08-322-742-19
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                                                                               Query Match
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                                     0;
Length 2337;
                                                                                                                                                                                                                                                                                 APPLICANT: Harbour, Eric
APPLICANT: Hattori, Jiro
APPLICANT: Hattori, Jiro
APPLICANT: Miki, Brian
TITLE OF INVENTION: MICROSPORE-SPECIFIC REGULATORY ELEMENT
WINHER OF SHOUDHIES: 8
CORRESPONDENCE ABURESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 33;
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                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                     2;
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Score 13.4; DB 5; Length 579;
Pred. No. 1.1e+02;
0; Mismatches 1; Indels
                    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 COMPUTER: HP Vectra 486/33 SOFTWARE: ASCIT Text.
CURRENT APPLICATION DATA:
FPLING DATE: PCT/US96/05320A FILING DATE: April22, 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               KEFERENCE/DOCKET NUMBER: 1488.014 PC01
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 371-2500
TELEFAX: (202) 371-250
TELEFAX: (202) 371-250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 3, 2002, 08:07:11
Job time: 42191 sec
                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              36,688
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 TCAAACTGATTAGGG 460
                                                                                                                                                                                                                                                                                                                           NAME: Eric K. Steffe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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PCT-US96-05320A-1664
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APPLICANT: J. Craig Venter
TILE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome,
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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TITLE OF INVENTION: MICROSPORE-SPECIFIC REGULATORY ELEMENT WIGHBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                     COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA: DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,198
FILING DATE: 01-APR.1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.4; DE Pred. No. 72; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 33229/236/P1H1
TELECOMMUNICATION INFORMATION:
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PCT-0596-05320A-1664
; Sequence 1664, Application PC/TUS9605320A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences
; APPLICANT: 9410 Key West Avenue
APPLICANT: 9410 Key West Avenue
... APPLICANT: COCKVIIIe, MD 20850
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/345,756
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
Johns Hopkins University
720 Rutland Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltimore, MD 21205
United States of America
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERESTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, STEPHEN A. REGISTRATION NUMBER: 2
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                               STREET: 3000 K Št
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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APPLICANT:
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APPLICANT:
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Gaps

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Perfect score:

Sednence:

OM nucleic

Run on:

Scoring table:

Searched:

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Database

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AA249381 135 bp mRNA EST 11-MAR-1997 13441.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA 5', mRNA sequence.
AAA249381.1 GI:1880285
                                                                                                                                                                 AQ928124 kPC1-21-2
AL547240 AL554340
BF23803 601811750
AI513102 GH01393.3
BG718674 60265951
AL520879 AL520879
AL559329 AL559329
BE73598 601 505358
AL556646 AL556646
BI115704 602866051
AL556646 AL5689
AL510747 Terrandon
AL52534 AL52534
AL525534 AL525534
AL525534 AL525534
AL525534 AL525534
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BG382488 298399 MA
AW774157 EST333240
AQ091462 HS_3016_B
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/Organism="Homo sapiens"
/Organism="Homo sapiens"
/Ob_xref="taxon:8606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
Xho1; mRNA was purified from human fetal hearts (8-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145)
Liew,C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNASS from human fetal heart (1997)

(Unpublished (1997)

Contact: Liew CC

Department of Laboratory Medicine and Pathobiology

University of Toronto

Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
                       BG639721
BG639722
BB647969
AL134134
BF944889
BF944887
BF944887
BF90411 AQ692029
                                                                                                                                         AA141880 (AW390923 P
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PORMARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
PORWARD: 5' CCAGTGAATTGTAATACGACTCACTATAAGGGC
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                              AL134134
BF944889
BF927805
BF944887
BF490411
AQ692029
AA141880
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BF238039
AI513102
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BF347028
AL520879
AL559329
BE735986
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BI115704
AL536089
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AL525534
AL551791
W18183
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BG382488
AW774157
AQ091462
                                   BG639722
BF947969
                                                                                                                                                         AW390923
AQ928124
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Fax: 4169785650
human.
source
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AA249381
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 LOCUS
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BF331466 QV1-HT051
BF376314 CM0-TN003
BF367020 PM0-GN001
BF367003 PM0-GN001
D44620 HUMSUPY017
BF77419 ILS-IT002
AW750028 PM2-BF064
BF944885 CM1-NN019
AW248379 AS20521.5
F05463 HSCOBH041 n
F12193 HSC36H081 n
                                                                                                       (without alignments) 50.427 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                         2002, 21:47:57 ; Search time 3835.7 Seconds
                                                                                                                                                                                                                                                                22703874
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                      11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA249381
BF551466
BF7370314
BF367020
BF367003
D44620
BF72419
AW750028
BF944885
FW248379
FW248379
                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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em_gss_vrt:*
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                   Homo sapieus
Eukaryota, Merazoa; Chordata; Craniata; Vertebrata: Euteleostomi;
Eukaryota; Merazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soarcs, F., Brentani, R.R., Reis, E.F., de Souza, S.J. and
Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following UKL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl+CMO&t2-CMO-TN0039-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF367020 375 bp mkNA EST 24 NOV-2000
MPG-CNV0118-130900-003-e09 GN0018 Homo sapiens CDNA, mRNA Sequence-
BF367020
                                                                                                                                                                                                 BF376314 356 bp mRNA EST 24-NOV-2000 CM0-TN0039-210800-507-c05 TN0039 Homo sapiens CDNA, mRNA sequence.
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Ludwiq Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
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Pred. No. 4e+02;
0; Mismatches 0; Indels
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Seq primer: puc 18 forward
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High quality sequence stop: 356
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BF376314.1 CI:11338339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
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1 (bases 1 to 160)

Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstenh, A., deofiveira, P. S., Bucher, P., Jongeneel, C. V., O' Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
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QV1-HT0517-020400-142-a08 HT0517 Homo sapiens CDNA, mKNA sequence.
BF351466
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Suo Paulo-SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shorgun sequencing of the human transcriptome with ORF expressed sequence tags
                                  adaptor-primer. EcoRI adaptors were ligated, followed digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

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            CDNA was synthesized using a XhoI-Oligo dT
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                                                                                                                                                                                                                                                   Length 135;
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+55-11-2707001
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/u. a.v. / /u.canism="Homo sapiens" / /u.a.v. / /u.canism="Homo sapiens" / /u.canism="Homo sapiens" / /u.canism="Homo sapiens" / /u.canism= /u.
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Contact: Shinji Hadano
Japan Science and Technology Corporation, NeuroGenes Project, ICORP
Univ. of Tokai School of Med.
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Tel: 81-463-91-6095
Fax: 81-463-91-4993
                                                                                                                                                                                                                                                                                                                                                                                           Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following UR.
(http://www.ludwig.org.br/Scripts/gethtml2.pl?tl=PM0&12=PM0-GN0018-
040900-002-A08&t3=2000-09-04&t4=1)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
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                                                       Shotgun sequencing of the human transcriptome with ORF expressed
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HUMSHPY017 Human brain chNA Homo sapiens cDNA clone 003, mKNA
Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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High quality sequence start: 12
High quality sequence stop: 76.
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                                                                                                                                                                                                                                                                                                                                                                  Tel: +55-11-2704922
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/db_xref="taxon:9606"
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/dev_stage="Adoult"
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/site_2: SmaI; A mini-library was made by choning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
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                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mass. 1 to 375)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Baria,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpsofludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-PMO&t2~PMO-GN0018-
130900-003-e09&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 375.
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GN0018 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
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Ludwig Institute for Cancer Research
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                 BF367020.1 GI:11329071
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1 (bases 1 to 427)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Brunstehn,G.H., Carvalho,A.F., Matsukuma,A., Baia G.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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Fax: +55-11-2707001
Fax: +55-11-2707001
This sequence stop: br he FAPESP/LICR Human Canrest Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-fl.5xt2-11.5-IT0027-12100-322-b06413-2000-12-12xt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                     BF772419 427 bp mRNA EST 12-JAN-2001
LS-TT0027-121200-322-b06 IT0027 Homo sapiens cDNA, mRNA sequence.
BF772419
BF772419.1 GI:12120319
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Ludwig Institute for Cancer Research
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/db_xref="taxon:9606"
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/clone_lib="Human brain cDNA"
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/organism="Homo sapiens"
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/dev_stage="Adult"
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Advastage "Adull"

Anote—"Organ: breas; Vector: pucl8; Site_1: Smal; Site_2:

Smal; A mini-library was made by cloning products derived

from CMESTES PCK (U.S. Letters Parent application No. 196

716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector: Reverse transcription of tissue

mKNA and CDNA amplification were performed under low
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.K., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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PM2-BF0546-281299-003-f07 BT0546 Homo sapiens CDNA, mKNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 594)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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88.9%; Score 16; DB 11;
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                              Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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This sequence as derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following UKL
Fucher. Wave, ludwig, org.br/scripts/gethtml2.pl?tl=CM1&t2=CM1-NN0193-191000-484-908&t3=700-10-19244=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence Stop: 166.
Location/Qualifiers
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                     BF944885 166 bp mRNA EST 22-JAN-2001
CM1-NN0193-191000-484-g08 NN0193 Homo sapiens cDNA, mRNA sequence.
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2820521.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820521 5',
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1 (bases 1 to 166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
/clone_lib="NN0193"
/dev_stage="Adult"
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Hong/Rubin Laboratory cNNA Library Arrayed by: The I.M.A.G.E. Consortium (LIANL) DNA Sequencing by: Berkeley MGC Sequencing project Cloue distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.igov/Dbrp/Image/Aimage/Aimage Aimage and a Scores: PHRED from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center Phrash suite. PolyTr Identification: patMatch.pl from BerKeley http://www.qenome.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Norgan: Lung; Vector: poTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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( bases 1 to 269)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlqatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
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1 (bases 1 to 238)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 238
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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
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Pred. No. 7.5e+02;
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                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM4 row: G column: 18
High quality sequence stop: 188.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKNA
                                                                                               Unpublished (1999)
Other_ESTs: 2820521.3prime
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HSC0BH041 normalized in:
c-0bh04, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.6%;
94.1%;
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F05463.1 G1:669279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 ACATCAAGTGATTGGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and its expression
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Best Local Similarity
Matches 16; Conserv
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us-09-785-904-3.rst

FEATURES

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/organism="Homo sapiens"
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KINASE-3 ALPHA ;, mRNA sequence.
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Location/Qualifiers
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Matches 16; Conserv
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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H14295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="total brain"
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/dev_stage="3 months old"
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/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient; tissue_type=total brain;
/solate=muscular atrophy patient; tissue_type=total brain
/solate="total brain"
/solate="to
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 301)

Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C., Devignes Auffray,C., Devignes, A.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B., Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Poullot,Y., Sebastiani-Rabaktchis,C. and Tessier,A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F12193 301 bp mRNA EST 13-MAR-1995
HSC36H081 normalized infant brain cDNA Homo sapiens cDNA clone
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Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-36h08
Seq primer: (-21)M13_universal.

Location/Qualiflers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
Genexpress-Genethon
Genethon Centre de recherche sur le Genome Humain
1,rue de l'internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 269;
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/sex="Female"
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Pred. No. 7.7e+02;
0; Mismatches 1;
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                                                                                                                                                                                            Email: genexpress@genethon.fr
Single read.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.6%;
ilarity 94.1%;
Conservative
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F12193.1 GI:706535
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Fax: 33160778698
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Best Local Similarity
Matches 16; Conserv
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F12193
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BASE COUNT

ORIGIN

δ g MEDLINE COMMENT

FEATURES

JOURNAL

TITLE

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

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/clone="th="normalized infant brain cDNA"
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/note="organ: brain; vector: lafmid BA; Site_1: HindIII;
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isolate=muscular atrophy patient; tissue_type=total
isolate=muscular atrophy patient; tissue_type=total
isolate=muscular atrophy patient; tissue_type=total
isolate=muscular atrophy patient; tissue_type=total
isolate=muscular atrophy patient; total muscular
lisolate=muscular atrophy patient; total muscular
isolate=muscular atrophy patient; total muscular atrophy patient;
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Rucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., M., Hultman, M., Rolfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Merck EST Project
Unpublished (1955)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: brain; Vector: pT773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; lst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stops: 179
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1920 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H14295 345 bp mRNA EST 10-JUL-1995
ym63b06.rl Soares adult brain N2b4HB55Y Homo sapiens CDNA clone
IMAGE:163571 5' similar to SP:KG3A_RAT P18265 GLYCOGEN SYNTHASE
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Washington University School of Medicine
4444 Forest Park Parkway, Box #501, St. Louis, MO 63108
Tel: 414 286 1800
Frax: 414 286 1800
Email: estewatson.wustl.cdu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 7.9e+02;
0; Mismatches 1;
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Score 15.4; DB 11;
Pred. No. 8.2e+02;
); Mismatches 1;
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BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualitiers
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Other_ESTs: SD04846.5prime
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 360)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Sinpson, D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-2707001
Email: asimpsondludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following UKL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-CMl&t2=CMl-NN0193-
301000-505-905&t3=2000-10-30&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF947972 360 bp mRNA EST 22-JAN-2001
CM1-NN0193-301000-505-905 NN0193 Homo sapiens CDNA, mRNA sequence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sac Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with OkF expressed
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20202663
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/db_xref="taxon:9606"
/clone_lib="NN0193"
/dev_stage="Adult"
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High quality sequence stop: 360.
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One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798

Fax: 510 486 6798

Faxi 510 486 7898

Faxi 510 
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:7227"
/clone="spo4846"
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Eukaryota; Melazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryyota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
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Db 379 CATCAAAGAGATTCGCG 363

Search completed: April 2, 2002, 21:48:01 Job time: 10826 sec

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April 2, 2002, 22:49:16; Search time 366.19 Seconds (without alignments) 42.142 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	M. tuberculosis ma	DNA for M. tubercu	Mycobacterium tube	M. tuberculosis ce	DNA for M. tubercu	BCG deletion regio	Neisseria gonorrhe	Neisseria gonorrho	Neisseria gonorrhe	N. gonorrhoeae 1gt	Lipo-oligosacchari
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	Query Match Length DB ID	650	650	1535	1535	1535	12412	1368	1779	1779	5859	5859
	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	85.6	85.6	85.6	85.6	85.6
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DMp53 tumour suppr C10-E15 DNA fragme C10-E12 DNA fragme Streptococcus pneu CFE 28 coding seq S. pneumoniac deri Streptococcus pneu Streptococcus pneu Human colon caucer Hepatitis C virus Hepatitis C virus	Arabidopsis thalia Mouse neuropeptide DNA encoding human Non-A, non-B hepat 5 'UTK/CORE/ENV/NS1 Human cytokine alp BAC containing rep HCC envelope regio Aspergillus oryzae DNA encoding a hum phibacin PSBX orf Phibacin PSBX orf Phibacin PSBX orf TATA-binding prote Drosophila TATA-bi ding prote Cas mays DNA fragm Neisseria gonorrhe MEKK3 CDNA. Mis s Probe #13262 for g Probe #13262 for g Probe #13262 for g Murine bone morpho Murine homologue t	ene. ge survival; vaccine; S. Ra (ATCC 25177). Penter mammalian cells - useful in vaccines to protect
AAA220 AAQ20 AAAQ20 AAAX19 AAH90 AAAX96 AAAX96 AAAX96 AAAX96 AAAX96	AAC34516 AAC46912 AAC64069 AAC64069 AAC640691 AAC130387 AAC12298 AAC12298 AAC13285 AAC12298 AAC13286 AAC13386 AAC133329 AAC33329 AAC33329 AAC33329 AAC33329 AAC33329 AAC33329	ALIGNM ALIGNM Survival g survival g t; macropha therapy; d strain H37 strain H37 on. ium tuberci ium tuberci
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M. tuberculosis, to induce a passive immunity and prevent disease
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                A DNA molecule (AAT3358) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT33556) obtd. by ligating M. tuberculosis genomic DNA fragments into paluescript II vector and screening recombinant E. colistrains for HeLa cellinvasive clones. It can be incorporated into a vector and used for prodn. Of recombinant macrophage survival protein, which is useful ir vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule (tuberculosis the ability to enter mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to survive within macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to
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                                                                                                                                                                                      100.0%; Score 18; DB 17; Length 650; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                               tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                            Indels
                                                                                                                                                      Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                       Cellular uptake protein; vaccine; infection;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 14; 82pp; English.
Claim 7; Page 45; 67pp; English
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                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                               AAV18649 standard; DNA; 650
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                                                                                                                                                                                                                                              1 catgccgtcgtattgctg 18
                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis
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                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9805784-A1
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                                                                                                                                                                                                                                                                                                                                                            03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                 DNA for M.
                                                                                                                                                                                                                                                                                                                                       AAV18649;
                                                                                                                                                                                                                                                                                                      AAV18649/c
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                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a secreted protein, a cytophasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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                                                                       Length 650;
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                       DB 19;
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                                                                    Score 18; DB :
Pred. No. 1.9;
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100.0%; Pred. No. 2;
ive 0; Mismatches
                                                                                                                         Mismatches
Sequence 650 BP; 123 A; 258 C; 185 G;
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1..1535
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                    AAQ89200 standard; DNA; 1535 BP
                                                                 ch
1 Similarity 100.0%; P
18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Lucal Similarity 100.0%;
Matches 18; Conservative 0
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                                                                                                                                                                        1 catgeoglogicatidetg 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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22-NOV-1996

AAT33656

RESULT 4

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Mycobacterium tuberculosis DNA \cdot confers ability to enhance uptake of therapeutic ayents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein frayment, which confers on M. tuberculosis an ability to enter meammalian cells and to survive within macrophages. The protein can be used in a varcine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                  DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 Other;
                                                                                                                                                     Cellular uptake protein; vaccine; infection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCG deletion region 3 and flanking sequences.
                                                                                                                                                                                                                                                               /*tag- a
/note- "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2;
Mismatches
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100.0%; Pred. No.
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1..1534
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AAV18647/c
ID AAV18647 standard; DNA; 1535 BP.
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(CORR ) CORNELL RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                   97WO-US13056
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                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                   03-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chong P, Riley LW;
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                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                    12-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT33537;
                                                 AAV18647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT33537/c
                                                                                                                                                                                                                             Key
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                  οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A DNA molecule (AAT33656) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The encoded protein sequence is given in AAW03301. The DNA was obid. by ligating W. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cellinvasive clones. The DNA includes 2 separate coding regions (see also AR733657-58) coding for the cell entry (AAW03302) proteins. It can be used to produce the cellular uptake proteins used as vaccines or to facilitate uptake of other materials, e.g. therapeutic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                             Cellular uptake; cell entry; macrophage; passive immunisation; vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1535;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= macrophage survival protein
                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 18; DB 17;
100.0%; Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                            /product= cell entry protein 886..1535
                                                                                                                                                                                                  M. tuberculosis cellular uptake gene region.
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                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                            BP
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/label= ORF-1
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/label= ORF-2
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                                                                                            AAT33656 standard; DNA; 1535
     1074 CATGCCGTCGTATTGCTG 1057
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                                                                                                                                                                    (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                          181..810
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WO9626275-A1

Key

CDS

29-AUG-1996

20-FEB-1996; 22-FEB-1995;

Riley LW;

BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.

RESULT

δλ

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Gaps

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DB 19; Length 1535; Indels

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Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
treatment; Neisseria infection; meningitis; septicaemia; gonorrhea; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria gonorrhoeae complete ORF61 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ12075 standard; DNA; 1779 BP
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Bost Local Similarity
Matches 16, Conserv.
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                                  30-APR-1999;
                                                                                                                                                                                                                      Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-OCT-1999
                                                                                                                                                25-FEH-1999;
                                                                        31-JUL-1998;
02-SEP-1998;
                                                                                             02-SEP-1998;
09-OCT-1998;
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                                                                                                                       09-OCT-1998
                                                                                                                                   09-OCT-1998
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                                                                                                                                                                                                                                                                                                                                        This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region casults in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT33535 and AAT33536) have also been detected. Identification involved Screening a BCG cosmid library with a radiolabeted probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of a virulent, or a virulent, mycobacterial phenotype. Determination of a virulence requires the detection of the presence or absence of presence or absence of absence of absence of absence of absence of absence or absence or absence or absence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                  Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria gonorrheae ORF 311 partial DNA sequence SEQ ID NO:1289.
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                                                           /*tag= a
/note= "BCG delta l deletion region"
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                                  Location/Qualifiers
1406..10673
                                                                                                                                                                                                                                                                                                                       Example 1; Fig 3; 66pp; English.
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          Mycobacterium bovis strain BCG
                                                                                                                                                                     95US-0390878.
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                                                                                                                                                                                               (PATH-) PATHOGENESIS CORP.
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Best Local Similarity 100.
Matches 18; Conservative
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                                                                                                                                                                                                                                               WPI; 1996-393419/39.
                                                                                                                                                                                                                        Mahairas GG,
                                    Key
misc_feature
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85.6%; Score 15.4; E 94.1%; Pred. NO. 49; ive 0; Mismatches

DB 21; Length 1468; Indels

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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ55473 represent polypeptides. AAZ54577 to AAZ54576 and AAZ55673 represent polypeptides. AAZ54577 to AAZ54576 and AAZ55673 represent promisers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection du: to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or or raise antibodies. They may also be used to screen for agonists or antiagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Galeotti C, Grandi G, 1
, Pizza M, Rappuoli K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 709; 1453pp; English.
                                                                                                   98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
99WO-US09346.
                                                                                                                                                                                                                                                            98US-0103794
                                                                                                                                                                                                                                                                                          98US-0103796
                                                                                                                                                                                                                                                                                                                                 9905-0121528
                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-062150/05.
P-PSDB; AAY74908.
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, Mora M; Scarselli M;

Masignani V, Scalato E, S

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represent novel Neisseria meningitis and N. gonorrheae polynucleoides and polypeptides. AAX54537 to AAX54576 and AA254616 to AAX55473 represent Per Per Primers used in the exemplification of the present invention. The polypeptides, the polynucleoides, antibodies and compositions of the Invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the nanificature of medicaments for treating or preventing infection due to be used to Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antigonists, which may themselves have use as antibocterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                  AA253015 to AA254546, AA254577 to AA254615, and AAY74253 to AAY75941
                                                                                                                                                                                               Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycosyltranslerase; lipo-oligosaccharide; lgt gene; LOS locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1779 HP; 367 A; 478 C; 599 G; 335 T; 0 other;
                                                                                Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB
Pred. No. 50;
0; Mismatches
                                                                                                                                                                                                                                                 Claim 7; Page 712-714; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tay= b
/note= "poly-G tract"
1491..2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Localion/Qualifiers
                                                                               Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrhoeae strain F62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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/product= LgtA
699..715
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/product= LgtC
2499..2508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 85.6%;
Best Local Similarity 94.1%;
Matches 16; Conservative
99US-0121528.
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                                                 (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                   vaccines and diagnostics
                                                                                                Pizza M,
Venter JC;
                                                                                                                                                  WPI; 2000-062150/05.
                                   (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. gonorrhoeae lqt
                                                                                                                                                                   P-PSDB; AAY74911
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                                                                                Fraser C, Ga
Petersen J,
Tettelin H,
25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT'14061;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences AA211972-212358 represent open reading frames (ORFs) of Neisseria meningitidis and N. gonorrhoeae which encode antigenic proteins (see AAY38499-Y38944). The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.4; DB 20; Length 1779; pred. No. 50; 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                      Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1779 BP; 367 A; 478 C; 599 G; 335 T; 0 other;
                                                                                                                                                                                                                      Grandi G, Masignani V, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                        Claim 9; Page 175; 524pp; English.
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98US-0094869.
98US-0099062.
98US-0103749.
98US-0103794.
                                                   98GB-0019016.
97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
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ilarity 94.1%;
Conservative (
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                      98WO-IB01665
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98GB-0000759
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                        (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                       P-PSDB; AAY38618
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02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
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                     09-OCT-1998;
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                                                                                                      18-NOV-1997;
                                                                                                                                                         14-JAN-1998;
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                                                        01-SEP-1998
                                                                                      14 - NOV - 1997
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AA253673 RESULT

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Gaps

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Indels

Length 1779;

DB 21; .; H 445..1491

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WO9640971-A1
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                                                                                                                                                                                      Buczala SL,
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CDS
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                                                                                                                                                                                                                                                                                                The lgt locus (AAT14061) of Neiserria gonorrhoeae F62 contains 5 open reading frames, 1gth, 1gtb, 1gtC, 1gtD and 1gtE, coding for 5 glycosyltransferases (see also AAR9131-15) involved in gonococcal lipooligosaccharide (LOS) biosynthesis. The sequence was constructed from 2 clones isolated from an F62 gene bank in lambda-200 following screening with plasmid pR10p1. 3 of the coding sequences contain poly-G tracts that make them susceptible to premature termination. The lgt coding sequences can be used for prodn. of recombinant LGT glycosyltransferases that are utilised in biosynthesis of LOS useful in vaccine prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                           Nucleic acids encoding glycosyl transferase(s) - used in the diagnosis of infection with Neisseria and for the biosynthesis of oligo:saccharide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipo-oligosaccharide (including polyglycosyltransferase) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyglycosyltransferase; N-acetylglucosaminyl transferase; N-acetylgalactosaminyl transferase; lipo-oligosaccharide; ss.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5859 BP; 1411 A; 1462 C; 1661 G; 1325 T; 0 other;
                                                                                                                                                                                                                        P-PSDB; AAR91311, AAR91312, AAR91313, AAR91314, AAR91315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                85.6%; Score 15.4; DB 17;
94.1%; Preu. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
/note= "poly-G tract"
3322..4335
                                              /*tag= g
/note= "poly-G tract"
4354..5196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1..381
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria gonorrhoeae ATCC 33084.
                                                                                                                                                                                                                                                                                 Claim 1; Fig 2g-m; 81pp; English.
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                   /*tag= f
/product= LgtD
3576..3586
                                                                           /*tag= h
/product= LgtE
                                                                                                                                          95WO-US12317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 atgccgtcgtattgctg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.6
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                             (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                 WPI; 1996-200924/20.
                                                                                                                                                                                                 Gotschlich EC;
                                      misc_feature
                                                                                                      WO9610086-A1
                                                                                                                                                             26-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1997
                                                                                                                        04-APR-1996
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          CDS
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                poly:glycosyl:transferase - isolated from N. gonorrhoeae, catalyses the addition of both Glenac and Galnac di:saccharide(s) units to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A lippoligosaccharide-encoding gene region (AAT49230) of Neisseria gonorrhoeae ATCC 33084 includes a coding sequence for a novel Neptylytocsyltransferase (PGTase) (AAM06576) that catalyses the addition of both Girnka and GalnAc disaccharides to a single galactose molecy. The products (AAW06577-80) of the other coding sequences of this region are not identified. The PGTase gene can be obtd. using standard techniques and incorporated into a vector to allow produ. of the PGTase in transformed host cells. The enzyme is useful in the synthesis of oligosaccharides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW06576, AAW06577, AAW06578, AAW06579, AAW06580
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                         /product= polyglycosyltransfarase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transfer of at least 2 saccharide units using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMp53 tumour suppressor gene (genomic DNA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NEOS-) NEOSE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA53978 standard; DNA; 27425
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/*tam
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4354..5196
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                                             2342..3262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnson KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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The sequence is that of a DNA fragment encoding a non-A non-B (NANB) hepatitis-specific antigen polypeptide, it can be used to produce the polypeptide recombinantly. It is derived from the DNA clone C10-E15. It can be used to dive PCR primers which are capable of detecting NANB hepatitis with high accuracy. See also AAQ20617-Q20629 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-A, non-B hepatitis-specific antigen polypeptide - for detection of hepatitis virus gene or antibody directed against virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C10-E12 DNA fragment encoding NANBH-specific antigen polypeptide.
                                                                                                                                                                                                                         Non-A, non-B hepatilis-specific antigen polypeptide - for of hepatitis virus gene or antibody directed against virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 742 BP; 129 A; 217 C; 209 G; 187 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kohara M;
                                                                                                                              Kohara M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Pred. No.
                                                                                                                              Toyoshima A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local ion/Qualitiers
                                                                                                                                                                                                                                                                                 Claim 18; Fig 18; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
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             90JP-0413844.
90JP-0180889.
90JP-0339589.
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90JP-0180889.
90JP-0339589.
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                                                                                                                              Yamaguchi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 CATGCCGTCGTATTG
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                                                                                           (TOFU ) TONEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                      P-PSDB; AAR20723
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                               09-JUL-1990;
30-NOV-1990;
                 20-DEC-1990;
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30-NOV-1990;
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                                                                                                                              Maki N,
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                                                                                                                                                                                                                                                                                                                                                metazoan invertebrate organisms, such as insects and worms, or cultured carls, resulting in p53 expression or mis-expression. The cultured carls, resulting in p53 expression or mis-expression. The cultured carls, referably a planmaceutical agent or a pesticide, that or molecules, preferably a pharmaceutical agent or a pesticide, that modulates p53 activity. The genetically modified organisms or cells are also useful for studying p53 activity by detecting the phenotype caused by the expression or mis-expression of the p53 protein in the insect. The method additionally comprises observing a second insect having the expression or mis-expression of the p53 protein, where the causes the expression or mis-expression of the p53 protein, where the second animal additionally comprises a mutation in a desired gene and differences between the-pfenotype of the first and second identifies the desired gene as capable of modifying the function of the gene central for identifying other genes modulating the cells are also useful for identifying other genes modulating the function of, or interaction with the p53 gene.
                                                                                                                                                                                                                                         Novel p53 tumor suppressor gene encoding a protein useful for genetically modifying metazoan invertebrate organisms, such as insects for screening compounds of pharmaceutical use or a pesticide
                                                                                                                                                Keegan KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                Ollman MM, Young LM, Demsky MR,
C, Larson JS, Robertson SA;
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Best Local Similarity 94.1%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                     Example 7; Page 80-89; 98pp; English
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             13-MAR-2000; 2000WO-US06602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ20926 standard; DNA; 742
                                                   99US-0268969
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                                                                                                                                                Platt DM, Olli
Kopczynski C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-A non-B hepatitis virus
                                                                   23-FEB-2000; 2000US-0184373
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                                                                                                          (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                        WPI; 2000-638178/61
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                                                   16-MAR-1999;
                                                                                                                                                Buchman AR,
Friedman L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1992
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RESULT 13 AAQ20926/c

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Gaps

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Indels

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Length 742;

DB 13; 77;

for detection

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The present sequence encodes the Streptococcus pneumoniae filty-four homologue (ffh) protein, which is a component of the protein secretory apparatus in bacteria, and the bacterial homologue of the eukaryotic Signal Recognition Particle. Fith proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of Ffh protein by identifying mutations in the Ffh gene, or determining Ffh protein or mRNN expression levels due to an infection of an organism with the Ffh gene. They can diagnose the stage and type of infection. Ffh proteins are also useful for screening for compounds which affect activity of the protein or surface or inhibition of the protein function. These can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance (agonist) Ffh activity, in addition to direct administration of Ffh
                                    The sequence is that of a DNA fragment encoding a non-A non-B (NANB) hepatitis-specific antigen polypeptide, it can be used to produce the polypeptide recombinantly. It is derived from the DNA clone C10-E12. It can be used to give PCR primers which are capable of detecting NANB hepatitis with high accuracy. See also AAQ20617-Q20629 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Streptococcus pneumoniae Fifty-Four Homologue (Ffh) polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of Streptococci infections, which cause otitis media, sinusitis and conjunctivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae; "ffh, fifty-four homologue; antibacterial; infection; otitis media; conjunctivitis; bacteraemia; sinusitis; pleural empyema; endocarditis; meningitis; ds.
                                                                                                                                                                                                                     Length 932;
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                                                                                                                                                            Sequence 932 BP; 173 A; 276 C; 257 G; 226 T; 0 other;
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                                                                                                                                                                                                                     DB 13;
78;
                                                                                                                                                                                                                   83.3%; Score 15; DB 100.0%; Pred. No. 78; cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAX19484 standard; DNA; 1569 BP.
         Claim 15; Fig 15; 78pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae.
                                                                                                                                                                                                                             Query Match 83.3
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                   438 CATGCCGTCGTATTG 424
                                                                                                                                                                                                                                                                                              1 catgccgtcgtattg 15
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                                                                                                                                       AAQ20922-020926
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direct administration of antisense sequences to prevent expression. Ffh proteins (administration of antisense sequences to prevent expression. Ffh proteins (administered directly, in a vector and as a vaccine) and antibodies induce an immune response to immunise and prevent disease. Diseases diagnosed, prevented or treated include: bacterial infections, especially Streptococcus pneumoniae infections, which cause otitis media, conjunctivitis, bacteraemia, sinustits, pleural empyema, endocarditis and especially menigitis. Fft proteins, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial
                                                                                                                                                                                                                                                                                                                                  infection.
                             5555555555555x8
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Sequence 1569 BP; 479 A; 297 C; 382 G; 411 T; 0 other;

Gaps ; Length 1569; Indels .; DB 20; 81; 0; Mismatches Score 15; Pred. No. 83.3%; Query Match 83.3 Best Local Similarity 100. Matches 15; Conservative

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completed: April 2, 2002, 22:49:19 9219 sec Search com Job time: Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 12, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Run on:

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TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
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Pred. No. 0.81;
); Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                    US-08-248-839C-5
US-08-248-839C-1
US-08-128-839C-7
US-08-146-715-1
US-08-146-715-1
US-08-362-670B-10
US-08-333-576C-12
US-08-333-576C-12
US-08-808-324-10
US-08-808-324-10
US-08-808-344-10
US-08-808-344-10
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US-08-808-324-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Riley M.D., Lee W.
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100.0%;
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.
Matches 18; Conservative
                                                          FILING DATE:
CLASSIFICATION: 435
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Sequence 5, Appli
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24.647 Million cell updates/sec
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Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-464-052-5
US-08-461-002-5
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US-08-461-002-1
US-08-103-84-09-1
US-08-103-84-08-1
US-09-103-84-08-1
US-09-103-84-08-1
US-09-103-84-08-1
US-08-112-387-8-1
US-08-112-387-8-1
US-08-683-426-7
US-08-683-426-7
US-08-683-426-7
US-08-683-458-1
US-08-683-458-1
US-08-683-458-7
US-08-478-1408-1
US-08-449-093A-18
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US-08-923-772-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351203 seqs, 113238999 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                            OM nucleic - nucleic search, using sw model
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Maximum DB seq
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Perfect score:
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-464-052-1
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 CATGCCGTCGTATTGCTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
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                                                                                                                                                                                                                                                                     650 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
CURRENT APPLICATION DATA:
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                                                                CLASSIFICATION: 536
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                                               FILING DATE:
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US-08-464-052-1/c
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US-08-689-411-5/c
Sequence 5, Application US/08689411
Patent No. 6224881
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: CELLULAR UPTAKE OF WCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                 APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.81;
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                                                                                                                                                                                   ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
CITY: Rochester STATE: No. Work COUNTRY: U.S.A.
ZTATE: N.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
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                         Sequence 5, Application US/08461002
Patent No. 6214543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-5
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CLASSIFICATION: 435
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CITY: Rochester
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ZIP: 14603
          US-08-461-002-5/c
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Sequence 1, Application US/08464052;
Patent No. 6008201;
GENERAL INFORMATION:
APPLICANT: HIVE OF INVENTION: DNA Molecule Encoding for Cellular;
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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NAME: Goldman, Michael L.
REGISTRATION UNBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
CITY: Rochester
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTATION NUMBER: 30,727
REFERENCE/COCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1500
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/464,05:
                                                                   APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-689-411-5
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ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                           NAME: Goldman, Michael L.
REGISTRATION NUMHER: 30,727
REPRENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/09863
                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                          Floppy disk
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 18; Conservative
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EDNESS: double
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                                                                                                   ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                New York
: U.S.A.
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                 STREET: CALLE
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PCT-US94-09863-1/c
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                                                              STATE: Ne
COUNTRY:
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APPLICANT: RIJEY, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      RESULT 5
US-08-461-002-1/c
US-08-461-002-1/c
Sequence 1, Application US/08461002
Sequence 1, Application US/08461002
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
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                                                                   Gaps
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                         DB 3; Length 1535;
                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERNCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
               Query Match 100.0%; Score 18; DB 3;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HAIGTAVE, DEVANS & DOYLE
STREET: Clinton Square, P.O. Box 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ROCHESCO
STATE: New York
COUNTRY: U.S.A.
2.PP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 1, Application US/08689411

; Patent No. 6224881

; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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TTY: Rochester
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps
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Pred. No. 0.84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
COMPUTER: 1BM PC: compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30.727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
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OTHER INFORMATION: CDC 1551; OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g US-09-103-840A-2
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GENERAL INFORMATION:
APPLICANT: FEBSIESCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHYER, Owen R.
APPLICANT: WHYER, Owen R.
APPLICANT: WHYER, OWEN R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 2436-2007.00
CURRENT APPLICATION NUMBE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATCH IN VOI. 2.1
SEQ ID NO ID NO
                                                                        APPLICANT: WHITE, OWER R.
APPLICANT: FASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: WIBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
SOFTWARE: PATENLIN Ver. 2.1
SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 18; DB 4; Length 4403765; llarity 100.0%; Pred. No. 1.1; Conservative 0; Mismatches 0; Indels 0;
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Patent No. 554553
GENERAL INFORMATION:
APPLICANT: GOLSCHICH, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCCANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09103840A; Patent No. 6294328
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                                                   APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity
Matches 18; Conserv
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Best Local Similarity
                    GENERAL INFORMATION:
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TYPE: DNA
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Patent No. 5700683

GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Floor
STREET: Floor
CITY: San Francisco
STATE: California ...
COUNTRY: USA
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                                                                                                                                                                                                                                                                                     Length 1535;
                                                                                                                                                                                                                                                                                  100.0%; Score 18; DB 5; Length 15
100.0%; Pred. No. 0.84;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPASSONS
SOFTWARE: PSTENDIN PC-DOS/MS-DOS
SOFTWARE: PSTENDIN DATA:
CURKENT APPLICATION DATA:
FILING DATE: 17-FEB 1995
CLASSIFICATION: 435
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NAME: Hunter, Tom
RECISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09103840A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) US-08-390-878-18
                                                                           STRANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PCT-US94-09863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1074 CATGCCGTCGTATTGCTG 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 catgccgtcgtattgctg 18
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                                     1535 base pairs
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
SEQUENCE CHARACTERISTICS
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                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Patentin Release #1.0, Version #1.25
                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 5859 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 201 487-5800
TELEFAX: 201 343 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conner at ive
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ 10 NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
 NUMBER OF SEQUENCES:
                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 16: Conset.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: COS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: F62
                                                                                                                        07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                    STATE: Ne
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Matich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-683-426-1
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APPLICANT: GOLSCÂLLICA, EMLI C.
TITLE OF INVERTION: GLYCOSYLUTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLLGOSACCHARIDES, AND GENES ENCODING THEM
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.4; DB 1; Length 5859; Pred. No. 19;
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                                                                                                                                                       COMPUTER: FLORM:
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORY disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: TEM PC-1005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOTE: July 7, 1994
CLASSIFICATION: AND ATS
NAME: Jackson Esq., David A.
RECISTRATION: NUMBER: 26, 742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 443-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CRARACTERISTICS:
LENGTH: 5859 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Neisseria gonorrheae
                                                        ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 94.1
Matches 16; Conservative
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3322..4335
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4354..5196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2342..3262
                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445..1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                                                             STATE: New Jersey COUNTRY: USA ZIP: 07601
                                                                                               Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: F62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-312-387B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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QQ ò

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APPLICANT: GOLSCHIECH, Emil C.
TITLE OF INVENTION: GLYCOSYLCHANNEERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 5859;
                                                                                                              COMPUTER READOLLE FORM:
MEDITIM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-100S/MS-100S
SOFTWAKE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85,68; Score 15,4; 194,14; Pred, No. 19;
                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRAFION NUMBER: 26,742
REFERENCE/DOACKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Klauber & Jackson STREET: Klauber & Jackson STREET: All Hackensack Avenue CITY: Hackensack STRTE: New Jerscy COUNTRY: USA Z.P.: 07501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Neisseria quiotrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/U8683426
Patent No. 5705367
GENERAL INFORMATION:
STREET: 411 Hackensack Avenue
CITY: Hackensack
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Sequence 1, Application US/08683458

Sequence 1, Application US/08683458

Patent No. 5798233

Patent No. 5798233

Patent No. 5798236

CENERAL INFORMATION:

APPLICANT: Gotschlich, Emil C.

APPLICANT: Gotschlich, Emil C.

APPLICANT: Gotschlich, Emil C.

TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: GLYCOSYLCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: Hackensack Avenue

CITY: Hackensack
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MEDIUM TYPE: Floppy disk
COMPUTER: ihm PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC 'COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION 197A:
APPLICATION 197A:
APPLICATION NUMBER: US/08/683,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.6%; Score 15.4; D
94.1%; Pred. No. 19;
live 0; Mismatches
                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION INTE:
APPLICATION INTE:
APPLICATION INTE:
CLASSIFICATION: 536
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095B
FELECOMMUNICATION INFORMATION:
TELEFAX: 201 343-1684
INFORMATION FOK SEQ 10 NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Neisseria gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (yenomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db - 2796 ATGCCGCCTATTGTG 2812
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COTHER INFORMATION: 19tB
US-08-683-426-7
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New Jersey
COUNTRY: USA
New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN: F62
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Sequence 7, Application US/08683426
Sequence 7, Application US/08683426
Sequence 7, Application US/08683426
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.4; DB 1; Length 5859; Pred, No. 19;
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LOCATION: 1..381
COTHER INFORMATION: 91ys (91ycy1 tRNA syntetase beta chain)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/683,426
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
FILING DATE: September 26, 1994
CLASSIFICATION: 536
ATTORNEY FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1-095B
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684
TELEC: 13351
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LIENGTH: 5859 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Neisseria gonorrheae
STRAIN: F62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: UNKNOWN MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.6%;
94.1%;
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LOCATION: 4354..5196
OTHER INFORMATION: 19tE
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OTHER INFORMATION: 19tD
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OTHER INFORMATION: 19tA
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OTHER INFORMATION: 19tC
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Best Local Similarity 94.1'
Matches 1f; Conservative
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LOCATION: 3322..4335
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LOCATION: 445..1491
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NAME/KEY: CDS

US-08-683-426-1

RESULT 14

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CURRENT APPLICATION DATA:

RILING DATE:
FILING DATE:
CLASSIFCATION:
A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05,1994
FILING DATE: September 26, 1994
APPLICATION NUMBER: 08,1994
APPLICATION NUMBER: 08,1994
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCEOCOMMUNICATION INFORMATION:
TELEPAN: 201 343-1684
TELEPAN: 1959 base pairs
TYPE: nucleic acid
SEQUENCE CHARACTERISTICS:
LENGTH: 5599 base pairs
TYPE: nucleic acid
SEQUENCE: UNKNOWN
TOPOLOGY: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: DNA (genomic)
HYPOLECULE TYPE: DNA (genomic)
HYPOLECULE TYPE: ON (GENOMIC)
HYP
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Best Local Similarity 94.1%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0;
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CCATION: 2342.3262
COCATION: 2342.3262
COTHER INFORMATION: 1gtC
FEATURE:
NAME/KEY: CDS
CTHER INFORMATION: 1gtD
FEATURE:
NAME/KEY: CDS
LOCATION: 3322.4335
CTHER INFORMATION: 1gtD
COTHER INFORMATION: 1gtD
COTHER INFORMATION: 1gtE
US-08-683-458-1
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Search completed: April 3, 2002, 08:12:53 Job time: 42533 sec

Run on:

MO

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AL457086 T. brucel
AQ55568 H. 5522_A
BI34257 371350 MA
AQ370996 HS_5034_B
AW58445 EST366915
BGB88511 1024058B0
AZ829376 2M0107F04
AU114159 AU134159
BGB60192 1024068A0
AU21224 AU21323
BH110072 RFC1-24-3
AQ250765 T15M3-T7
BF942570 604 CDNA
AW940855 CH22341.3
AW940855 GR2341.3
AW940855 GR2341.3
AW340855 GR2341.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                      AL203162.1 G1:7861507
GSS: genome survey sequence.

GELrandon niqroviridis.

Teltrandon niqroviridis.

Teltrandon niqroviridis.

Teltrandon niqroviridis.

Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopteryqii; Neopterygii; Teleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetrandontidermes;

Tetrandontidae; Tetrandon.

I (bases 1 to 779)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                         nigroviridis genome survey sequence T7 end of clone
library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                 14-MAY-2000
                                                                                                                                                                                                                                                                                                        ALIGNMENTS
         AV834783
AI105888
                                          AQ085253
BE428498
                                                                            AQ646244
BE024649
BE024887
                                                                                                                                                      AQ555508
BI343257
AQ370996
                                                                                                               AA314278
BG733499
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BG858511
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AU134159
                                                                                                                                                                                                                           AU213234
BH110072
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AW940855
                                                                                                                                      BF769545
                                                                    BE442482
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                                                                                                                                                TA72B03P
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                                                                                                                                                                                                                                            AQ250765
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779 bp
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Unpublished
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Tetraodon 1
148A13 of Seguence.
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RESULT 1
CNS02LR5/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
AL201570 Tetraodon
AU060300 AU060300
AU06178 AU06178
N93955 2b74f01.s1
AU061934 AU061934
AQ179545 HS_317_A
BE775420 MY -02-G
AW934449 EST340426
AN934449 EST340426
AL403700 GH32265.5
BE777156 MY -25-B-0
BE77116 MY -25-B-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL203162 Tetraodon
                                                                 (without alignments) 50.427 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      April 2, 2002, 21:48:01; Search time 3835.7 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                      22703874
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                     residues
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                         using sw model
                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    11351937 seqs, 5372889281
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AU060300
AU061778
N93955
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AQ179545
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A1403760
BE777156
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                                                                                                                           IDENTITY_NUC Gapox 1.0
                                                                                                           catgccgtcgtattgctg 18
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em_gss_fun:*
em_gss_hum:*
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Maximum DB seq length: 2000000000
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em_gss_rod:*
                                                                                      US-09-785-904-4
18
                                                                                                                                                                                                                                                        em_estfun:*
em_esthum:*
em_estinr:**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_estro:*
em_estov:*
em_htc:*
gb_est1:*
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gb_htc:*
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t     4 others
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Tetraodon nigroviridis genome survey sequence T7 end of clone
145H15 of library G from Tetraodon nigroviridis, genomic survey
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
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/db_xref="taxon:99883"
/clone="145415"
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Pred. No. 3.8e+02;
0; Mismatches 1;
                                                                                                     /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="148A13"
                                                                                                                                                                                                                                                                                                                         91.1%; Score 16.4; DB 13;
94.4%; Pred. No. 3.6e+02;
tive 0; Mismatches 1;
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/clone_lib="G"
/note="Genoscope s
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ilarity 94.48;
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Lortyostellum.

Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

El (bases 1 to 332)

Morio,T., Urushihara,H., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Yoshihams,J., Maeda,M., Takeucchi,I., Ochiai,H. and Tanaka,Y.

Milliams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

Developmental cDNA in Dictyostellum discoideum

Lu Unpublished (1998)

Contact: Hideko Urushihara

Institute of Biological Sciences

University of Tsukuba

3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan

Email: d402hu@sakura.cc.tsukuba.ac.jp

PROJECT = Dictyostellum discoideum cDNA project in Japan.
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                                                                                                                                                                                                        Eukaryotta, Mycerczoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 252)

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Witshina, B.N., Pi.M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. Developmental CDNA in Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU061778 332 bp mRNA EST 20-MAY-1999
W1061778 Dictyostellum discoldeum SL (H.Urushihara) Dictyostellum
discoldeum cDNA clone SLF846, mRNA sequence.
AUG60300 252 bp mRNA EST 20-MAY-1999 AUG60300 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum cDNA clone SLJ109, mRNA sequence.
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Unpublished (1998)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba Sciences
3-3-10 Ten-nodai, Tsukuba Ibaraki 305, Japan
Email: d402hu@sskura.cc.csukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
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/organism="Dictyostelium discoideum"
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Pred. No. 9.2e+02;
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/db_xref="taxon:44689"
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1 (bases I to 468)

1 (bases I to 468)

1 (bases I to 468)

2 (bissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Moris, M., Paranes, C., Rifkin, L., Menling, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Neg, J., Treevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                 /strain="AX4"
/db_xref="teaxon:44689"
/clone="sLF846":
/clone_lib="Dictyostellum discoideum SL (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Insert Length: 480 Std Error: 0.00
Seq primer: mbD.REGA+ET
High quality sequence stop: 223.
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                                                                                                                                                                                                        Length 332;
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/clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                   /organism~"Dictyostelium discoideum"
                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                      Score 15.4; DB 10
Pred. No. 9.6e+02;
); Mismatches 1
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Location/Qualifiers
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                                                                                                                   /dev_stage="slug
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94.1%;
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N93955.1 GI:1266264
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SOURCE

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1 (bases 1 to 490)

Norlo, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yushida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Unpublished (1998)
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Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library. Soares fetal heart NbHH19W." 102 c 7 4 g 168 t 6 others
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AU061934 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
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/dev.stage-"sluq"
119 c 79 q 152 L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Tsukuba 1baraki 305, Japan 3-3-10 Ten-modai, Tsukuba, Ibaraki 305, Japan Email: d402huesakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project in Japan. Lotation/Qualifiers
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Pred. No. 1e+03;
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Institute of Biological Sciences
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/db_xref-"taxon:44689"
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88.9%;
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ilarity 94.1%;
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MY-02-G-06 PinfestansMY Phytophthora infestans cDNA, mkNA sequence.
BE775420
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Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_vref="Plate=3177 Col=7 Row=I"
/clone_"Plate=3177 Col=7 Row=I"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm: Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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Kamoun, S., Habber, P.T., Sobral, B.W.S., Nuss, D. and Govers, F. Initial assessment of gene diversity for the comycete pathogen phytophthora infestans based on expressed sequences Fungal Genet. Biol. 28 (2), 94-106 (1999)

Contact: Govers F
                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/strain="DDR7602, Al mating type"
/db_xref="taxon:4787"
/clone_lib="PinfestansMY"
/dev_stage="4-week old vegetative, non-sporulating mycellum in synthetic medium"
/lab_host="E. coli, strain DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potato late blight agent.
Phytophthora infestans
Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 508;
                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3177 row: I column: 7
Class: BAC ends
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Pred. No. 1e+03;
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/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; Total RNA was isolated from mycelium of P. infestans DDR7602 cultured for 4 weeks in synthetic medium. EST clones were named by their position in the microtiter plate, preceded by the prefix MY (for mycelia) and the successive number of the microtiter plate (e.g. MY-06-A-04)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 Lo 530)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hausen,T., Craven,M.B., Bowman,C.L., Ahn,S., Rouning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue (Uppblished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solamales; Solamaceae; Solamum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST340426 tumato fruit mature green, TAMU Lycopersicon esculentum cDNA clone cLEF40A23 5', mRNA sequence.
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Prod. No. 1e+03;
0; Mismatches 1; Indels 0;
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/clone="chek40023"
/clone=lib="tomato_fruit_mature_green, TAMU"
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/enltivar "TA496"
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Pred. No. 1e+03;
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1. .530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l. 640
/organism="Drosophila melanogaster"
/db_xref="taxon:727"
/clone="GH2325a:727"
/clone="GH2325a:727"
/clone="In Drosophila melanogaster head pryr2"
/sex="male and female"
/sex="male and female"
/dev_stage="adult"
/lab_host="H5 - alpha"
/note="Organ: head; Vector: porr2; Site_1: EcoR1; Site_2:
XhoI: Sized fractionated coRNs were directly ligated into porr2: plasmid cDNA library."
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MY-25-B-07 PinfestansMY Phytophthora infestans CDNA, mKNA sequence.
BE777156
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Wageningen University
Binnenhaven 9, P.O.Box 8025, 6700 EE, Wageningen, The Netherlands
                                                                                                                                                                  Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda; Insecta; Pterygota: Metazoa: Arthropoda: Tracheata: Brachycera: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Maccomorpha: Ephydroidea: Drosophilidae: Drosophila. I (bases 1 to 640)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsaug,G., Endis,S. and Rubin,G.M.
BDCP/HHMI Drosophila EST Project
Unpublished (2001)
      AI403760 640 bp mRNA EST 19-APR-2001
GH23265.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH23265 5prime, mRNA sequence.
AI403760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytophthora.

1 (bases 1 to 671)
Kamoun,S., Hraber,P.T., Sobral,B.W.S., Nuss,D. and Govers,F.
Initial assessment of gene diversity for the oomycete pathogen
Phytophthora infestans based on expressed sequences
Fungal Genet. Biol. 28 (2), 94-106 (1999)
                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA One Cyclotron Rd, Berkeley, CA 94720, USA Exa: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.bcrkclcy.cdu plate: 232 row: F column: 5
High quality sequence stop: 438.
Location/Qualifiers
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Phytophthora infestans
Eukaryota: stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 640;
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Pred. No. 1.1e+03;
0; Mismatches 1;
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                                                                                                                                                         Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                      Contact: Stapleton, M.
                                                                                                A1403760.1 GI:4246847
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Contact: Govers F
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Best Loca! Similarity
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BE777156
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AUTHORS
TITLE
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KEYWORDS
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A1403760
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/strain="Denty Computer Integrals"
// Alb xref="texton:4780".
// Alb xref="texton:4787"
// Alb xref="texton:4787"
// Alb xref="texton:4787"
// Alb host="E. col; strain DH5-alpha"
// Alb host="E. col; strain DH5-al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       normalized, Lambda Zap II Note-"Vector: pluseript II SK-; Site_I: Ecokl; Site_2: XhOI; This library, constructed by John Davies and Jeffrey mcDermott, combines cDNAs from CC-1690 cells grown to mid-log plase in Tap-N (30 min, 1hr, 4hr), TAP-S (30 min, 1hr, 4hr), TAP-P (4hr, 12hr, 24hr), NO3 to NH4 (30min, 1hr, 4hr) and NH4 to NO3 (30min, 1hr, 4hr). PolyA mkNA was purified from each sample, pooled and cDNA synthesisked. The cDNA was directionally cloned into lambda Zap II (SIratagene) in the ECORI (5') and XhORI (3') SILUS.
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Chlamydomonas reinharditi.
Eukaryota, Viridiplantav, Chlorophyta, Chlorophyceae, Volvocales;
Chlamydomonadaceae, Chlamydomonas.
1 (bases 1 to 2051)
Chasses 1 to 2051)
Chasses I to 2051)
Accisemanta, Davies, J., Foderspiel, N., Harris, E., Hauser, C.,
Lerebyre, P., McDermant, L.P., Shrauer, J., Silllow, C. and Stern, D.
Analyses of the Chlam, the mass reinharditi Genome: A Bodel,
University and System for Analyzing Gene Function and Requiring in
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/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                /organism="Phytophthora infestans"
Tel: 31 317 483 138
Fax: 31 317 483 412
Email: Francine.Govers@medew.fyto.wau.nl.
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Unpublishen (2000)
Contact: Charles Hauser
DCMB Bax 91000
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Tel: 919-613-8159
Fax: 919-613-8177
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Best Local Si
Matches 16;
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us-09-785-904-4.rst

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 128)
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                                                                                                                                                                                     AV834783 575 bp mRNA EST 22-JUN-2001
AV834783 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
Spontaneum top three leaves adult, heading stage Hordeum vulgare
subsp. spontaneum cDNA clone bahl5n23, mRNA sequence.
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cb01a01_p1 ZF adult heart library Danio rerio cDNA 5 prime, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Razuhiro Salo
Research Institute for Bioresources
Okayama University, Barley Germphasm Center
Chuo 2-20-1, Kursahiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp,
Salo, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare subsp. spontaneum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
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Expressed Sequences from The Adult Zebrafish Heart
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/dev_stage~"adult, heading stage"
160 c 154 g 119 t
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100.0%; Prod. No. 1.7e+03;
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Hordeum vulgare subsp. spontaneum
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/clone="bahl5n23"
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1 (bases 1 to 575)
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Query Match
Best Local Similarity
Matches 15; Conserv
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/db_rref="taxon:10090"
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/note="vector: pfaRBAC1; Site_1: BamH1;
/note="vector: pfaRBAC1; Site_1: BamH1;
/note="vector at the BamH1 sites using MboI partially digested male C57BL/6J
DNA."
pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Broad of et al. (1996) Genome Research 6: 791-806."

461 c 551 g 294 t 167 others
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other, GSSs: RPCI-24-333FS. TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library and a state of the state of th
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Contact: Mark C. Fishman
Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 617726580
Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
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M12799 COTYNCHOL AF360732 Brucella AF114243 COTYNEBAC E00311 DNA CODING

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08-SEP-2000 DATA molecule encoding for cellular uptake of mycobacterium tuberculosis and uses thereof Patent: US 6008201-A 5 28-DEC-1999;
Location/Qualifiers
1. 650 PAT 6008201 AR096715 650 bp UNA Sequence 5 from patent US 60 AR096715 AR096715.1 GI:10025753 Unclassified. 1 (bases 1 to 650) Riley, L.W. Unknown. Unknown. RESULT 1
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Riley, L.W. and Chong, P.
Riley, L.W. and Chong, P.
DNA molecule fragments encoding for cellular uptake of
Mycobacterium tubérculosis and uses thereof
Patent: 18 6224881-A 5 01-MAY-2001;
Location/Qualifiers
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Mycobacterium bovis BCG DNA flanking deletion region 3.
U35021
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Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                         Unclassified.

(bases 1 to 1535)
Riley,L.W. and Chony,P.
DNA molecule fragments enroding for cellular uptake of
Mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 101-MAV-2001:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lenqth 1545;
                                                                          Length 1535;
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100.0%; Pred. NO. 4.2e-78;
ive 0; Mismatches 0;
                                                                            38.9%; score 176; DB 6; I. 100.0%; Pred. No. 4.2e-78; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           Sequence 1 from patent US 6224881.
AR147694
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1. .1535
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544 c 458 g
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                     /∪rganism-"unknown"
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                                                                                                                                                      Joses 1 to 1604)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology,
                 Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 1604)

Mahairas,G. G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.

Molecular analysis of genetic differences between Mycobacterium

Molecular analysis of genetic differences between Mycobacterium

J. Bacteriol. 178 (5), 1274-1282 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (14-AUG-1997) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTU43540 3453 bp DNA BCT 14-AUG-1997
Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein
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Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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100.0%; Pred. No. 4.1e-78;
ive 0; Mismatches 0; Indels
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/db_xref="taxon:1765"
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Location/Qualifiers
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Matches 176; Conservative
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NSAVRRLLDRGRIGGFYLLISSEGERDNLTVLRGLLRLANDRDDDFDHYTDRVAHDLRY
AILDPSRLYDELCWARKHTDFERALRTIDWYRDNESWLASLKHAGGRYQDAGO"
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NSAVRRILDRGRIGETYLISSEGERDNLTVLRSLLRLMDRDPDDFDHVTDRVAHDLRY
AIDPSRLYDELCWAPKHTDFERALRTTIDWYRDNESWLASLKHAGGRYQDAGQ"
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VLLIDQDRNLYVSDGLAHGFLALQDNSTVMYLCSAEYNPQRQHTTCATDPTLASTRRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TILEAVRHGVRLHHISTDEVYGDLELDDRARFTESTPYNPSSPYSATKAGAUMLVRA
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7202. .2655
7001c-m3-4 copies in M. tuberculosis genome; Found in the rfb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv, tubers, Erdman, and many isolates; not found in M. smegmatis & M. avium."
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/db_xref="taxon:1773"
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150. 1139
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100.0%; Pred. No. 3.5e-78;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          /note="previously known as rfbB"
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1136. .1747
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150. .1139
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/yene="MT0098"
2280. 2873
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3002. 3772
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Actinomycetales; Corynebacterineae: Mycobacteriaceae;
Mycobacterium: Mycobacterium tuberculosis complex.

(bases 1 to 9281)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K.
Molecular analysis of genetic differences between Mycobacterium bovis BCG and virulent M. Dovis
J. Bacteriol. 178 (5), 1274-1282 (1996)
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Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Direct Submission
Submitted (29-AuG-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
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misc_difference replace(1400. .>9281,"")
/note="absent in related avirulent strain M. bovis BCG"

COUNT 1706 a 3191 c 2929 g 1453 t 2 others
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I (bases 1 to 9764)
Fleischmann, R. D., Alland, D., Eisen, J. A., Carpenter, L., White, O. Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J. F., Nelson, W.C., Umayam, L. A., Ermolaeva, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 egegggccacetttgaagccgtgctagccaaactggccgccccggcgcgaccaaccccg 337
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of 280 of the
                                                                                                                27-APR-1996
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                                                                                                                                 end.
                                                                                                                 BCT
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100.0%; Pred. No. 2.9e-78;
iive 0; Mismatches 0;
                                                                                                                                  'n
                                                                                                      MBDR3S1 9281 bp DNA
Mycobacterium bovis deletion region 3,
035017
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                                                                                                                                                                                                                 Mycobacterium bovis. Mycobacterium bovis
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AE006921 AE000516
AE006921.1 GI:138
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Best Local Similarity
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AE006921/c
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TITLE
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/translation="naknonrirnelitegleghytyapddaalaaklrastglege
vwrclrcgdpfalggpggrapedaplimrgaligniitrlgvrivkalvlalaam
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ayavloavesglemlikrwgeyfavvatsffeldevholakgitttrvytfsinvaav
vyiliskrlegevrggrkaydverrgeglldleraamlt"
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ELDGSGTVRGNIKPYRLYVGSKFSYKWKLFGLPYRATSRYTALKPRELVECSHPLGH
RWRWEFESLSPTLTRVTETFDYHAAGAIKNGLKFYEWTGFAKSNAAG1EATLAKLSDO
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PYVTANDIDAPVLTRAGTRFANAPIRALHADIMTAELDNAGFDAVVSNNAIHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLMHLTSWVACGMANRVKGKWEHSAPIKWP
PPOTLHELRSHVRALLDFGACIRRLLYGRVLVTWRAPV"
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="MT0095"
//gene="This region contains an authentic point mutation,
//oute="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact; similar to SP:
                                                                                                                                                                                                                                                                                           "(bases 1 to 9764)
"(c) Alland,D., Eisen,J.A., Carpenter,L., White,O.,
"(c) Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E.,
"(c) Rolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
"(c) Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
"(d) Il,J., Mikula,A. and Bishai,W.
"(d) Direct Submission
"(d) Direct Su
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/strain="CDC1551"
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/protein_id="AAK44321.1"
/db_xref="G1:13879145"
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/protein_id-"AAK44320.1"
/db_xref="GI:13879144"
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/note="clinical strain"
122. .1414
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/translation="mimulhpogdltpterarkrgittsnooydgmski.sgyltpoara
TFEAVLAKLAAPGATRNDDHTPVIDTPDAAAIDRDTRSQAGNHD51.AGLRALIAS
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TGRTDITELTLAGGPUNRLAEKGWTTHKNTHGHTEWLPPPHLDHGQ):HTNTFHHPERF
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Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not the result of a sequencing artifact; identified by doliments; putative, conserved hypothetical protein, authentic frameshift.
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                                                                                                                                                                                                                                                                                                                                                                                                              complement(8956, .9623)
/yone="MT0104"
/note="This region contains an authentic frame shift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9764;
                                                                                                                     /product="conserved hypothetical protein"
/protein_id-"AAK44326.1"
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                          /note="identified by Glimmer2; putative"
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    11. 10019
    /organism="Mycobacterium bovis BCG"

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100.0%; Pred. No. 2.9e-78;
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                                                                                                                                                                                           /db_xref~"G1:13879150
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                                                                                             /transl_table=11
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                                                                  /codon_start=1
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/gene-"MT0103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="Aak44323.1"
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5DLAGASGVDFNRFVGEVAASSARVLLRLLPVLTAC"
5105. .7390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIAQATTAGSFNHHASTVLQGCRGVPAAMWSEPAGAIRRHCATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cation-transporting ATPase, E1-E2 family"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleosidase/S-adenosylhomocysteine nucleosidase
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                                                                         by Glimmer2; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRYPLGCGTVGGPQMTAPSSA"
complement(7337. .8185)
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/codon_start=1
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/traislat on "mynodatrptndacodgonnsdilvvaroovlokugedladdulation-"mynodatrptndacodgonnsdilvvaroovlokugedladdulation-"mynodatrptndacopegevestislystycechesilalahevraracoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudacoperudaco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRTDJTDLTLACDPDNRLAEKGWTTRKNTHGHTEWLPPPHLDHGQPRTNTFHHHEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGPHLAPAPMANSI.PGQWTAHVTLARRVGGHQLGRALRIAGRPSR111GRFAGLRRWDG
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/note="ORF10; similar to MTCY336.13c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comprement(9571, >10019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(5612. .6478)
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7455. 18504
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/mute "Blob: similar to MICY316.15c"
                                                                                                                                                                                           4957. .5466
/note-"ORF6; similar to MTCY336.32c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6339..7007)
/note="ORFB: similar to MFCY336.16"
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GLLFSSGYTANLGAVVGLSGPGSLLVSDARSHASI.VDACRESRRRVVPHRDVDAVD
ARLRSRDGNAVVYTDSSAGSCLAPYREAHLIDAARPPILEY.WGGGRG
LLYELGLAGAPDVWTTTLSSAGSGGSVVLGFTPYRAHLIDAARPPILFDTGLAPAN
GAARAALRVLQARARNCOAVLHHAGELARMCGVAAVPDSAMVSVILGFPESAVAAAA
CLDGGVRVQGCFRPPTVPAGTSRLRTARASLNAGELELARRVLTDVLAVARR"
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DIMCVGRATTGGTLSLAATUCTADVAHTISAGAAGLMHGFYFMANPLACAVSVASVE
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VLANBAGLSQRGVPFSAAGGGISGPTRGTGINTVGFDASGLIQYAYAGAGLKLPRSS
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complement(1278 . 1850)
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adenosyImethionine-8-amino-7-oxononanoate
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3120. .4280

/gene="blof"

/gene="blof"

/foclambler="2.3.1.47"

/codon_start=11
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                              'db_xref="taxon:33892"
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GKPLTDHRVTTWPTIFNPWTYAGMAKLAVIAAKVITGRKLSRRPL"
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Stover,C.Kendall and Mahairas,G.G.
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        /protein_id="AAB96964.1"
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CLVFRLAPVGHTLINQLDTQASEEELGSTLCCALANRLRITK FDAANIAT TADAANLGPR
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SRSISSRRAGPLRPAGHGLATPRRRPHRHTTRPQTRHHPEQPAIRKHVTAKWLPDPPS
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/product="conserved hypothetical protein"
/product="d-"AAK45890.1"
/db_xref="G1:13881251"
/tcranslation="MLAKLAAPGATNPDDHTPVIDTTPDAAAIDRDTRSQAQRNHDGL
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AHHYSPASGRYPQATFDHGTPLALYHTRRTASPAQRTMLFANDKGCTKPGCDAPAYHS
QAHHVTAWTSTGRTDTTDTTLACDPDNRTAFKGWTTHKRTHGITFWLPPPHLDHCQPR
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Whole yenome comparison of Mycobacterium tuberculosis clinical and
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1. 17783 /organism-"Myrobacterium tuberculosis CDC1551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
2 (bases 1 to 17783)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Roloney, J.F., Nelson, W.C., Umayam, L.A., Ermolacva, M., Koloney, J.F., Nelson, W.C., Utterback, T., Weidman, J., Khouri, H.,
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                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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/db_xref="G1:13881252"
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/wene-"MT1622.1"
/note-"identified by Glimmer2; putative"
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/note-"identified by Glimmer2; putative"
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Gill,J., Mikula,A. and Bishal,W.
Direct Submission
Submitted (25-APR-2001) The Institute
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/db_xref="GI:13881253"
Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
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/note="clinical strain"
complement(104..826)
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/gene "MF1623"
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EGWAVSVPDHEGPKGLWGSPYEPGYRVLDGIRAALNSERVGLSPATPIGLWGYSGGGL
                                                             VAAFRLALPRIMLEFAGGREITLGDLGAKRGILGGINAVIVGNYLTTLGRPAEADLEL
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NEFIAPPMLGGLLSVLAVVASALMWOWREHREPDWAGLSIGLTTAAAIAAGVGALVV
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AGTARDDLGGYPAVDPSSNARTEALETPQAPVS"
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GLARVIKEHANDEGRQLLEQLTEMTTVDAVIRWAGRDMGDFLDEPLEDILSTPEVSHV
FGDTKLGSAVPTPPVLIVQAVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRSAHTGANSDLAHNLVTPDLNQFDDLPLESKR"
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                                                                                                                                                                                                                   'note="identified by Glimmer2; putative'
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complement(4063. .5430)
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                                                                                                                                                                                                                                                                                                                                                                              KTVLIPDQRAGCSLADSITPDELRAWKDEHPGAVVVSYNTTAAVKALTDICCTSSNA
VDVVASIDPDREVLFCPDQFLGAHVRRVTGRKNLHVWAGEGHVHAGINGDELADQARA
HPDAELFVPPEGGCATSALYLAGEGAPPAERVKILSTGGMLEAAHTTRARQVLVATEV
CMLHQLFRAAPEVDFRAVNDRASCKYMKMITPAALLRCLVEGADEVHUDPGIAASGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGARLDESVPGKWALTREGGHSRRRIVHAGGDATGAEVQRALQDAAGMLDIRTGHVA
I.RVLHDGTAVTGLL.VVRPDGCGIISAPSVILATGGLGHLYSATTNPAGSTGDGIALGL
WAGVAVSDLEFIQFHPTMLFAGRAGGRRPLITEAIRGEGAILVDRQGNSITAGVHPMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DI APRIDVVAAA I DARIKATGDPCVY LDARGI EGFASKPPTVTASCRAAGI IDVVRQP I P
VVPCAHY SCCGI VTVDVYGOTELLGI YAAGBVARTGI HGANRIASNSI LIEGI IVVGGRAG
KAAAAHAAAGGRSKATSSATWEPI SYTALDRGDLQRAMSRDASMY RAAAGLHRLCDS
LSGAQVRDVACRRDFEDVALTLVAQSVTAAALARTESRGCHHRAEY PCTVPEQARSI V
VRGADDANAVCVQALVAVC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"similar to GB:L20833 Sr:P30011 GB:L28105 P1D:310262 P1D:456041; identified by sequence similarity; putative"
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PID:1651334; identified by sequence similarity; putative"
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Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.
295586 AL123456
29586.1 GI:3261785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GP:608530; identified by sequence similarity; putative"
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thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.9%; Score 176; DB 100.0%; Pred. No. 2.6 ive 0; Mismatches
                                                                                                                        /qene="MT1630"
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                                                                                                                                                                                                                                /transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table !!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7468. .9051
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7468. .9051
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9021. .9908
                                                6419. 7468
/gene-"MT1630"
6419. 7468
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Matches 176; Conserv
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VERSION
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2117233.
                                                                                                Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 32437)

1 (class 1 to 32437)

1 (cole,S.T., Brosch,R., Barkhill,J., Garnier,T., Churcher,C., Takia,F., Badcock, K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S., Imalin,M., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,M., Rogers,J., Raplandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  betails of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.%anger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in Taparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon gaty, gty, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deciphering the biology of Mycobacterium tuberculosis from the
                                                      Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mycobacterium tuberculosis H37Rv"/strain="H37Rv" /db_xref="taxon:83332"/clone="Y336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .32437
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/strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence
Nature. 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(39. .2228)
/gene="Rv1565c"
complement(39. .2228)
/gene="Rv1565c"
                         Mycobacterium tuberculosis H37Rv
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/db_xref="taxon:83332"
/clone="Y48"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 32437)
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TITLE
JOURNAL
                                                             ORGANISM
                                                                                                                                                                                 REFERENCE
AUTHORS
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KEYWORDS
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probably exported has goAPV repeats at C-terminus, similar probably exported has goAPV repeats at C-terminus, similar to hypothetical M. leprae protein, to putative invasins 1,2(007390, 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_LISMO P21171. FASTA results, 049634 COSMID B1170 (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlapp. Thearse scereis 0.890"

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/transl_table-11
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                                                                                                                                                                                                                                        HIWSMSVQGOPYLAFTLLVAGGAYLLRRLFROPRAPYLRTMFVVLLSTI.TIASFIYAI
VAHHAYQATAYYNIFARAWELLAGALVGAVVPHVRWPMWLRTAVATAALAAILSCGAL
                                                                                                           /translation~"mltlspprppaltpepalppvtmgtrttgfyrholdglrgvala
Lvavphywpgrysggydyflalsgfppggkilraalnpdlslspiaevirlirrllpa
                                                                                                                                                                  LVVVLAGCALLTIAIQPQTRWEAFANQSLASLGYYQNWELASTVSNYLRAGEAVSPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2327. .3019)
/qene="Rv1566c"
/note="Rv1566c, (MTCY336.37), len: 230. Function: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site (PS00600). FASTATESULES, BIOA_MYCLE P4548 (436 ad) opt: 2534; E(): 0; 85.1%identityin 435 aa overlap. Also similar to other M. tuberculosis proteins e.g. MTCY227.12c, (449 aa). FASTA score: E():3.5e-16; 29.5%identity in 421 aa overlap. TBparse scoreis0.874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"possible RBS, AAGAGG, for Rv1566c" complement(3258. 3263) /note-"ASNI site: ATTAAT: probably linking fragments H3766"
/product="hypothetical protein Rv1565c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comptement (32%, 3543)
Adone-"Rv1567c"
complement (325%, 3543)
/gene="Rv1567c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2327. .3019)
/gene="Rv1566c"
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/gene="bioA"
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/gene="bioA"
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Wed Apr

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2 (bases 1 to 38380)
Parkhill, J.
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6. .956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="hycD"
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                                                                                                                                          REFERENCE
                                                                                                                                                             AUTHORS
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SOURCE
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VERSION
                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                       LAKLLVDITPAGLDTVFFSDSGSVSVEVAAKMALOYWRGRGIPGKRRLMTWRGGYHGD
TFLAMSICDPHGGMHSLWTDVLAAQVFAPQVPRDYDPAYSAAFEAQLAQHAGELAAVV
VEPVVQGAGGMRFHDPRYLHDLRDICRRYEVLLIFDEIATGFGRTGALFAADHAGVSP
                                                                                                                                                                                                                     DIMCVGKALTGGYLSLAATLCTADVAHTISAGAAGALMHGPTFMANPLACAVSVASVE
LLLGQDWRTRITELAAGLTAGLDTARALPAVTDVRVCGAIGVIECURPVDLAVATPAA
LDRGVWLRPFRNLVYAMPPYICTPAEITQITSAMVEVARLVGSLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="WKAATQARIDDSPLAWLDAVQRQRHEAGLRRCLRPRPAVATELD LASNDY.GG.SRHPAVIDGGVQALRIWGAGATGSRLYTGDTKLHQQFEAELAEFVGAAA GLLFSGGTANGAVGLGSGGSLLVASDARSHASLVDACRESRAVVYTPRRDVAVD AALRSRDEQRAVVTDSGYSLAPVRELLEVCRRHGALLLYDBAGGGTGTLLTLSGALGGYRGGRG LLYELGLAGAADVVMTTTLSKALGSQGGVVLGPTPVRAHLIDAARPFIFDTGLAPAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAARAALRVLQAEPWRPQAVLNHAGELARMCGVAAVPDSAMYSVILGEPESAVAAAA
CLDAGVKVGCFRPPTVPAGTSRLRTARASLNAGELELARRVLTDVLAVARR"
5806. .5835
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                                                                                                                                    WLTLIRDGQPIEVLDAMSSWWTAIHGHGHPALDQALTTQLRVMNHVMFGGLTHEPAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pyridoxal-phosphate attachment site (PS00599). FASTA results, BIOF_MYCLE P45487(385 aa) opt: 1971; E(): 0; 80.18 identity in 381 aa overlap. Also similar to MTCX10H4.32, FASTA score: E(): 5.5e.29;37.48 identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Nul569, (MTCY336.34c), biof, len: 386. Function: probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17582 CGCGGCCCACCTTTGAAGCCGTGCTAGCCAAACTGGCCGCCCCCCGGCGCGACCCAACCCG 17523
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Mycobacterium tuberculosis H37Rv complete genome; segment 5/162.
274410 AL123456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 32437;
                                                                                                                                                                                                                                                                                                                         /note="PS00600 Aminotransferases class-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00599 Aminotransferases class-11
pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                        pyridoxal-phosphate attachment site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trans]_table=11
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                                                                                                                                                                                                                                                                                                                                                                          /gene="bioF"
5101. .6261
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6258. .6938
                                                                                                                                                                                                                                                                                4541. .4654
/gene="bioA"
                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="bioF"
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/gene="bioF"
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Bacteria: Firmioutes Actinobacteria Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridae;
Mycobacterium: Mycobacterium tuberculosis complex.
Mycobacterium: Mycobacterium tuberculosis complex.

(bases 1 to 38380)

(cole, S. T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S. V., Eiglmeier, K., Gas, S., Barry 11, C.E., Tekaia, F., Badcock, K., Hasham, D., Brown, D., Chillinqworth, T., Connor, R., Davies, K., Levin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Roqers, J., Rutter, S., Seeger, K., Skelton, S., Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whilehead, S. and Barrell, B. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:1405752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="RY0084, (MTCY251.02), len: 316,hycb, similar to MTCD_ECOLI P16430 formate hydrogentyses subunit 4 (307 aa) FASTA scores, opt: 570, z-score: 591.6, E(): 2.1e-26, (33.8% identity in 305 aa overlap) and NUOH_ECOLI 933.03nandh dehydrogenase i chain h (325 aa) FASTA scores, opt: 207, z-score:220.7, E(): 9.5e-06, (26.5% identity in 260 aaoverlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atq. 9tq. or tdg) which is preceded by an upstream ribusome binding site sequence (optimally 5-13bp before the initiation codon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web. (UKL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) (DS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
Nature. 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mycobacterium tuberculosis H37Rv"
/strain="H37kv"
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/db_xref="SPTREMBL:010881"
Mycobacterium tuberculosis H37Rv.
                                             Mycobacterium tuberculosis H37Rv
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<1. .35889
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/transl_table=11
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gene

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/translation-"MOOPWINATHYOALLDAMVPLGTQCVLDVGCGOGLLAARLARRI
PYVTAVDIDAPVI.RRAQTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVYPGGTLAVVTFVTPSLRNGLWHLTSWYACGMANRVKGKWEHSAPIKWP
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RWHWETESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
                                                                                                                                             NAAVTGHRLLRGAIRAGGVALRALPOTDELAALAVDIAEVATUTLANSVVYDRFAGTA
VLHPDDASALGCCLGYVARASGIRSDARVEHPTIVLPITEIGAPISGIVLARYTVRRDEF
AASAALAQHIVESHTGPIEYAATLHPVGAPSSGIGIVEGWRGTIVHKVEIDVDGRITR
AKVVDPSWFNNPALPVAMADTIVPDFPLANKSFNQSVAGNDL"
                                                  RFSVAGETIVRLKARLMFVHRGIEKLFHGRPATAAVDLAERISGDTSAAHALAHSLAI
EDALGIELPHEVHRLRALIVELERLYNHAADLGALANDVGYSLANAHAQKIRENLLRR
RLVRHAHWPDWHPMRTDAGPAPEFTDTGAFPFLAVEGPGVYE1PVGPVHAGL1EPGHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337
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/codon_start=1
/transl_table=11
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/note="aaqqaq, potential rbs upstream of 16158. .6928
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/protein_id-"CAA88925.1"
/db_xref="C1:1405759"
/db_xref="SwISS-PROT:010886"
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0; Mismatches 0;
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/gene="Rv0089"
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AMGEWMGSGAOFGLGGLLANDALTVVMLVVIGIVGTLATAASIGY IDTELAIGHIDGR
SARLYGVITPAFICCAMVLAVCANN GOVIWVA LEATTVITAFITVGHKWTRTALEATWKY
VYCSVGIAVAFLGTVLLYRARDSGAAAAGALLANDILLEHAGLIDPGVARLAGGLLL
IGYGAKAGLFPFHYRLADAHSQAPAPVSALMSGVLLAVAFSVL KLRPI LDAYSGPAY
LRNGLLVVGLATLLVAVLMLTVTGDVKRMLAYSSMEHMGLIATAAAAGTTLATAALLL
LRNGLLVVGLATLLIANAVLMLTVTGDVKRMLAYSSMEHMGLIATAAAAGTTLATAAALLL

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VYLFLAGYPDRRVELEYVVPADNPEIRSLAYLSFPAGRFEREMADLYGIRPVGHPKPR
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ArtplikgTRDDRALIAVGTAVLAHARALVERAMAERAAGREAAGREATPLVNTASS
LLITAGLTLTARATTRUPVWLEPGVTINAVPARFAVVLIALFWHTYKLHAGOAAGFL
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LLFLGTVALTLAGIDTGTSFGGWGASETTIAALVEPTILLAVFALSIPAGSANLGAL
VASTIDHPGTVVSLAGVLAFVALVIVIVAETGRLPVDNPATHLELTWVHEAVVLEYAG
PRLAVVEWAAGWRLTVLALLANLFLPWGIAGAAPTALDVLTGVVAVAAKVAILAVLL
ATFEVFLAKIRLRVPELLAGSFLLALLAVTAAANFFTVGA"
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/note="Rv0085, (MTCY251.03), len: 220. hyce, similar to
/note="Rv0085, (MTCY251.03), len: 220. hyce, similar to
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/protein_id="CAA98922.1"
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/db_xref="SPTREMBL:010883"
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/db_xref="GI:1405755"
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/db_xref="GI:1405757"
/db_xref="SPTREMBL:010884"
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/product="hycP"
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(URL, http://www.sanger.ac.uk/Projects/M.tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M.tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old peen renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes implemented in TBpares (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G i C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where pussible we choose an initiation codon initiation which is preceded by an upstream ribusione binding site sequence (optimally 5-1 bp before the initiation codon). If this cannot be identified we choose in most upstream
                                                                                                                               Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes: Actinobacteriaceae;
Actinomycetales: Corynebacterineae; Mycobacteriaceae;
Actinomycetales: Corynebacterium tuberculosis complex.
Mycobacterium; Mycobacterium tuberculosis complex.
E. (Abases 1 to 43401).
S. I (Abases 1 to 43401).
Raris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Eiglmeler,K., Garles, C., Tekala,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
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Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skellon,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted on behalf of the Mycobacterium

Submitted (1.740-1998) Submitted on behalf of the Mycobacterium

Submitted (1.740-1998) Submitted on behalf of the Mycobacterium

tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome

Trust Genome Campus, Hinkton, Cambridge CB10 15A Unite de Genetique

Trust Genome Campus, Institut Pasteur, 28 rue du Docteur Roux,

75724 Paris Cedex 15, France B-mail: parkhill@sanger.ac.uk

On Jun 27, 1998 this sequence version replaced gi:2104370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence Nature. 393 (6685), 537-544 (1998)
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                                                                                         Mycobacterium tuberculosis H37Rv. Mycobacterium tuberculosis H37Rv
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   295390 AL123456
295390.1 GI:32
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TITLE
JOURNAL
ACCESSION
VERSION
KEYWORDS
                                                                                                                                      ORGANISM
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MEDLINE
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                                                                                                          SOURCE
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probable precursor of serine protesse. Has putative signal peptideat N-terminus and hydrophobic stretch at peptideat N-terminus three signatures typical of subtilase family: asparic acid active site (PS00136), histidine active site (PS00136), histidine active site (PS00138), serine active site (PS00138), FASTA results: 903863 SERINEPROTEASE (390 aa) opt: 241: E(): Results: 38:08 identity in 387 aa overlap), similar to mycylsfolo 29 (45.7% identity in 451 aa overlap)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        //codon_start=1
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VNAQGERISAFTLAGGRAVDYAAFGEAVYSLSIPEDIGTVNRLAGGRGS LPTSGTSYAAPV
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GTATTSIPALVAVFVTRKSTFGPSBRKALHITAPAGAATTLALAATLATASRRLRPGRN
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ADVALENGEWI AAALTAANLAAAVTGALLLRARSADTRRSLYFYI (*CLITTVATFYVA
ADVALENGEWI AAALTAANLAAAVTGALLLRARSADTRRSLYFYT (*CLITTVATFYVA
WILGGAYSAVRILULITWT"
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/note-"PSS00137 Serine proteases, subtilase tamily,
histidine active site"
2456. 2488
/yene-"Rv3449"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      611. .>43401
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1478. oorf
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DDHIAAIALFGNPSGRAGGLMSALTPQFGSKTINLCNNGDPICSDGNRWRAHLGYVPG
                                                                                                                                                                                                                                                       Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Bodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases | to 16384)
Fleischmänn, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, U., Peterson, J., Dedson, R., Gwinn, W., Hirkey, E., Peterson, J., Nelson, W.C., Unayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mkula, A. and Bishai, W.
Direct Submission
Submitted (12-APR-2001) The Institute for Genomic Research, 971
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
of 280 of the
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871. 1566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism∸"Mycobacterium tuberculosis CDC1551'
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Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 16384)
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section 246
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Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="serine esterase,
                                                                                                                     Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="CDC1551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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                                                                   G1:13883389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"MT3557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1624. .1863
/gene="MT3560"
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/gene="MT3560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /qene-"MT3557"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains
                      complete genome.
AE007160 AE000516
AE007160.1 G1:138
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DEFINITION
                                                                                                                                           ORGANISM
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                                               ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SWISS-PROT:006318"
/translation="MGAGALITAVVLLIALGAVWTPVAFADGCPDAEVTFARGTGEPP
                                                                     /translation="MPSPATTWLHVSGYRFLLRRIECALLFGDVCAATGALRARTTSL
ALGCVLAIVAAMGCAFVALLRPQSALGQAPIVMCRESGALYVRVDDVWHPVLNLASAR
                                                                                                                                         VVVGPAEDSSAQVLTAEQMILVATESGSPTYLLYGGRRAVVDLADPAVVWALRLQGRV
PHVVAQSLLNAVPEAPRITAPRIRGGGRASVGLPGFLVGGVVRITRASGDEYYVVLED
GVQRIGQVAADLLRFGDSQGSVNVPTVAPDVIRVAPIVNTLPVSAFPDRPPTPVDGSP
                                                                                                                                                                                                            GRÄVTTLCVTWTPAQPGAÄRVAFLAGSGPPVPLGGVPVTLAQADGRGPALDAVYLPPG
RSAYVAARSLSGGGTGTRYLVTDTGVRFAIHDDDVAHDLGLPTAAIPAPWPVLATLPS
GPELSRANASVARDTVAPGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLVLGGYSQGATVIDIVAGVPLGSISFGSPLPAAYADNVAAVAVFGNPSNRAGGSLSS
LSPLFGSKAIDLCNPTDPICHVGPGNEFSGHIDGYIPTYTTQAASFVVQRLRAGSVPH
LPGSVPQLPGSVLQMPGTAAPAPESLHGR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGRVGQAFVDSLRQQTGMEIGVYPVNYAASRLQLHGGDGANDAISHIKSMASSCPNT
                                                                                                             LIAATNANPQPVSESELGHTKRGPLLGIPGAPQLLDQPLAGAESAWAICDSDNGGSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                //orde="R.Y.351, (WTCY13E12.04), len: 247. Function: probable cutinase, similar to several, contains cutinase, serine active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU 050664 probable cutinase cy339.08c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCY13E12.05 (FASTA score: E(): 0; (59.2% identity in 211 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15964 ACGACCACACCCCGGTCATCGACACCCCCGATGCGGCCGCCATCGACCGCGCCACCC 16023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable cutinase precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                        /gene="Rv3450c"
/note="Ps00013 Prokaryotic membrane lipoprotein lipid
attachment site. 4228.
/note="possible RBS, GGAG, for Rv3450c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgcgggccacctttgaagccgtgctagccaaactggccgcccccggcgcgaccaaccccg 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 acgaccacaccccggtcatcgacaccacccccgatgcggccgccatcgaccgcgacacc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00155 Cutinase, serine active site, GGYSQG" 5165. .5168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 - APR - 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 176; DB 1; Leuylor
Pred. No. 2.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MTCY13E12.05), len: 226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transI_table=11
/producfe*hypothetical protein Rv3451"
/protein.id="CAB08717.1"
/db_xref="G1:2104374"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5165. .5168 - ......... serine active
/note="possible RBS, GAGG, for Rv3452"
5178. .5858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCT
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                                            /db_xref="SPTREMBL:006317"
                                                                                                                                                                                                                                                                                    complement(4049. .4081)
                                                                                                                                                                                                                                                                                                                                                                                                               4388. 5131
/gene="Rv3451"
4388. 5133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4388. .5131
/gene="Rv3451"
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/gene="Rv3451"
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/gene="Rv3452"
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/note="Rv3452,
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Best Local 9
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LOCUS
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CDS

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/product="ribosomal protein S4"
/protein_id="Aak47904.1"
/protein_id="Aak47904.1"
/brotein_id="G1:13883397"
/Lasslation="MaryTgPVTKSRRLRTDLVGGDQAFEKRPYPPGQHGRARIKES
EYLLOLOEKOKARFTYGWMEKOPRRYYEEAVRQPGKTGEELLKILESRLDBVIYRAGI
PRYRRAMRAGOVSHGHYWVNOGHYWVPSYRVGOYDIUDVRDKSLNTVPFQIARETAGER
PIPSWLQVVGEKOKULHQLPERAQIDVPLTEQLIVEYYSK"

COMPLEMENT (6706..7125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Lranslation-"marlygyddprdkrmeyaltyifgigrtrsneilaatgidrddr
Trblteeoliiilkhyieanlkvegdbrrevqadirrkieigcyogirhrrgmpyrgor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MPPAKKGPATSARKGOKTRRREKKNVPHGAAHIKSTFNNTIVTI
TDPQGNVIAAMSSGHVGFKGSRKSTPPAAQLAABNAARKAQDHGVRKVDVFVKGPGSG
RETAIRSLQAAGLEVGAISDVTPQPHNGVRPPKRRN"
complement (7129) . 7503)
ARTESDLLDIRNFGQKSIDEVKIKLHQLGLSLKDSPPSFDPSEVAGYDVATGTWSTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GP:2104383; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"similar to SP:P45810; identified by sequence similarity; pitative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to SP:P45812; identified by sequence similarity; putative" /codon_start=1
                                                                                                                                                                                                /note="similar to SP:P81288; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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Pred. No. 9.4e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table-11
/product="ribosomal protein S11"
/protein_id="AAK47905.1"
/db_xref="G1:13883398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //radus_table-11
/product="ribosomal protein S13"
/protein_id="AAK47906.1"
/db_xref="GI:13883399"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7129. .7503)
/gene="MT3567"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (7719. .7832)
/qene_"MY3567.1"
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/qene-"MT 3567.1"
                                                            complement(6092, .6697)
/gene="MT3565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKTNARTKKGPKRT LAGKKKAR"
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                                                                                                                                complement(6092. .6697)
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                                                                                                                                                                                                                                 similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MT3566"
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                                                                                                                                                                 /gene="MT3565"
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                                                                                                                                                                                                                                                                      /codon_start=
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                                           AYDEQDYAETEQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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/product="trna Aak47901.1"
/product="trna Aak47901.1"
/db_xref="col:13883394"
/db_xref="col:13883994"
/db_xre
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GEVTAGDIVPPAGVTVHNPGMHIATLNDKGKLEVELVVERGRGYVPAVQNRASGAEIG
RIPVDSIYSPVLKYYTXVDATRVEQRTPFDKLILDVETKNSISPRDALASAGKTLVEL
FGLARELNVEAEGIEIGPSPAFADHIASFALPIDDLDLTVRSYNCIKREGVHTVGELV
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INVTNAYSGSLAWTNSFTRLTKHYPGRVVPLGVNLAIALLUMEANWFDFLWTILGCYA
NCGMANVYNASDIGFNKYLLGLSPKTPEFRGMLYAINPVGFGSLLLAAGLSITYFF
GGLGAALQPYSPLVAIVTALWPPITAAAYRGKYLLRTHDGIDLPWYDEHGNPSAAV
ILCHVCHDDPERPDMALQCTHGAHVCSLCLSTDKQAEHVLPGLARAHIPGDQVP"
complement(3485. 4378)
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RPYAEKLITHAKKGALHNRREVLKKLRDKDVVHTLFAEIGPFFADRDGGYTRIIKIEA
RKGDNAPMAVIELVREKTVTSEANRARRVAAAQAKAKKAAAMPTEESBAKPAEEGDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /LTAINSTALLON-**MANDOYTINSESPTAADHDRITATRETLEDYTLRLAPRSYRRWPP
AVVGISALGGIAYLADFAIGANVGITWGTANALCGIAIFALVVEVYGLELAYYAARYN
IDLDLITREGSGRYGSVYRWIYEATFIFFIFFALEGSIMAQGIKLGLHIPLWAGYACS
TLIIFPLVYYGMKLYSQLOIMYTFIMLILMAAPEGYLLVSHPDSIGOFFSYAGKDGHG
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/protein_id="AAK47903.1"
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simlarity; putative"
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cellular uptake: cell entry; macrophage survival; vaccine;
passive immunisation; gene therapy; ds.
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Copyright (c) 1993 - 2000 Compugen Ltd
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DNA giving M. Luberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Myrobacterium Luberculosis infection

WPI; 1996-425086/42. P-PSDB; AAW02303

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis DNA - confers ability to enhance uptake of therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                    A DNA molecule (AAT3358) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT3355) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cellinvasive clones. It can be incorporated into a vector and used for prodn. of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule tuberculosis the ability to enter mammalian cells.
                                                                            protein (AAW02303) that confers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 cycygyccacctttgaagccgtyctayccaaactgyccycccccyycycyaccaaccccy 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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Mismatches 0
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/note= "stop codon not given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.50,
100.08; Pic
    Claim 7; Page 45; 67pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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/*tag=
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Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW47543
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\overset{\mathbf{A}}{\times}\overset{\mathbf{A}}{\times}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\overset{\mathbf{A}}{\circ}\ov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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acgaccacacceccgyteategacaccaccecgatgeggeegeeategacegegacacee 397
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibudies raised against it can be used to treat mammals already exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
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                                                                                                                                                                                                                                                                                                                                                                    Length 650;
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                                                                                                                                                                                                                                                                                     Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.6e-77;
                                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 176; DB 19; 100.0%; Pred. No. 4.6e-77;
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1..1535
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A DNA molecule (AAT33656) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The enter mammalian cells and to survive within macrophages. By igating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cellinasive clones. The DNA includes 2 separate coding regions (see also ART33657-58) coding for the cell entry (AAM02302) and macrophage survival (AAM02303) proteins. It can be used to produce the cellular uptake proteins used as vaccines or to facilitate uptake of other
                                                                                                                                                   Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                           materials, e.g. therapeutic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                       Conservative
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P-PSDB; AAW47541.
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Matches 176; Conserv
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                                                                                                                                                                                                                                                                338 acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                                                                                                                                                       Gaps
     macrophages. It encodes a polypeptide having a mol. wt. of about 50°55 kDa, pref. 52 kDa. The AA sequence represents a highly hydropholic proform with a hydropholoic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell entry; macrophage; passive immunisation;
                                                                                                                                              Length 1535;
                                                                                                                                                                      indels
                                                                                                   Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= macrophage survival protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis strain H37Ra (ATCC 25177).
                                                                                                                                            DB 16;
4.3e-77;
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/label= ORF-1
/product= cell entry protein
886.1535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M. tuberculosis cellular uptake gene region.
                                                                                                                                           Query Match
38.9%; Score 176; DE
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 17f; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                          BP
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/label= ORF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellular uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhance uptake of
                                                   cgcgggccacctltqaaqccgtgctayccaactggccgccccgggggggaccaaccccq 337
                                                                                               acgaecandecerquicategaeaeeaceeegatgeggeegeeategaeegegaeaeee 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an
                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines
       Length 1535;
                                                                                                                                                                                                                                                                                                 DNA for M. tuberculosis cellular uptake protein fragment.
                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis DNA - confers ability therapeutic agents e.g. antibiotics, also useful
                               ô
       Score 176; DB 17;
Pred. No. 4.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                           /*tag a
/miee= "stop conton not given"
                                                                                                                                                                                                                                                                                                                      Cellular uptake protein; vaccine; infection;
38.9%; Sco. 100.0%; Pred. No. ... 100.0%; Preds ... 0; Mismatches ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Pages 9-10; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CONN-) CONNAUGHT LAB LTD. (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                              AAV18647 standard; DNA; 1535
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Query Match
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                                                                                                                                             This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region results in an avirulance phenotype of the mycobacterium. 2 other deletion regions (see AAT33535 and AAT33536) have also been detected. Identification involved screening a BCG cosmid library with a
                                                                                                                            Gaps
ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect bacterial infection
                                                                                                                                                                                                                        BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
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0
                                                                                                        Length 1535;
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                                                                           Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "BCG delta 1 deletion region"
                                                                                                        38.9%; Score 176; DB 19;
100.0%; Pred. No. 4.3e-77;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                     BCG deletion region 3 and flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1406..10673
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                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium bovis strain BCG
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                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                              Conservative
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                                                                                                                     Similarity
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Matches 176;
                                                               occurrence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H37Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of the deletions are detected either by detecting the presence or absence of deletion junctions (see AAT33538-46), or by detecting the presence or absence or absence of the presence or absence of all the presence or absence of absence of the sequences contained within the detection. Deletion polypoptides are used as components of immunological assays and in vaccines.
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                                                                                                                                                                                                                                                                                                                                                                              Length 12412;
                                                                                                                                                                                                                                                                                             Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 3.7e-77;
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Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                   38.9%; SCC.
100.0%; Pre
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; Z000EP-0127688
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 176; Conserv
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03-AUG-2000;
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Tateishi N,
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are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lygine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum MP protein nucleotide sequence SEQ 1D NO:411
                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; vitamin; carbohydrate; aromatic compound; cofactor; polyketide; enzyme; ds.
                                                                                                                                                                     Gaps
                                                                                                                                                                    0;
                                                                                                                                                22; Length 1413;
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                                                                                                                    Sequence 1413 BP; 259 A; 350 C; 395 G; 409 T; 0 other;
                                                                                                                                                 DB 2
                                                                                                                                                                      Mismatches
                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                             4.0%; bcc-
100.0%; Pre/
0; )
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99DE-1031573.
99DE-1031592.
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99DE-1031428.
99DE-1031434.
99DE-1031435.
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99DE-1030476.
99US-0142101.
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99DE-1031478.
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                                                                                                                                                                                       Corynebacterium glutamicum
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                                                                                                                                                            Best Local Similarity 100.
Matches 18; Conservative
                                                                                                     European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200100843-A2.
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09 - JUL - 1999)

09 - JUL - 1999)

09 - JUL - 1999)
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08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
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AAF71958/C
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AAF71753 to AAF72380 encode the Corpuebacterium qlutamicum metabolic pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP nucleic acids are useful for the production of fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vilamins, cofactors, polyketides and enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases:
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nilarity 100.0%; Pred. No. 17;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA04886 standard; DNA; 1536 BP.
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990E-1042129.
2000US-0187970.
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99DE-1040766.
99DE-1040832.
99DE-1041378.
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99US-0148613.
99DE-1040764.
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99DE-1041396.
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               99DE-1032228
                            990E-1032229.
                                                                  99DE-1032922
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99DE-1032928.
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99UE-1032227
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Matches 18; Conserv
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31-AUG-1999;
31-AUG-1999;
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03-SEP-1999;
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14 -JUL-1999;
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03-SEP-1999;
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03-SEP-1999
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promoter

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at host cells. The present sequence is a coding sequence of B. pertussis. No name has been specified for the present sequence. The present sequence may be a housekeeping gene. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The present sequence is located within a pathogenicity island (see AAA64890) which also carries, a number of genes encoding proteins involved in the type III secretion system of B. pertussis. See AAA64890-AA64884 and AAB1411-B14146 for details of the coding sequences and provering identified in the pathogenicity island, of the present invention.
                                                                         Type III secretion system; virulence factor; pathogenicity island; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pTrp1-35 DNA encoding the 2,5-diketogluconate-reductase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides derived from Bordetella pertussis, useful for treating and diagnosing Bordetella infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 18; DB 21; Length 1536; 100.0%; Pred. No. 17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1536 BP; 248 A; 546 C; 560 G; 182 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2,5-Diketogluconate-reductase; ascorbic acid;
                                            Bordetella pertussis coding sequence # 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Pages 154-156; 165pp; English.
                                                                                                                                   Location/Qualifiers
1..1536
/*tag= a
/product= "Protein # 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Bollen A, Fauconnier A, Godfroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                  (ULBR ) UNIV LIBRE BRUXELLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN50261 standard; DNA; 1853
                                                                                                                                                                                                                                                                                                     98GB-0028217.
                                                                                                                                                                                                                                                                          99WO-EP10297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 ccgacggcgacctcaccg 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ccgacggcgacctcaccg 187
           02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                        Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                              WP:; 2000-452178/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              P-PSUB; AAB14148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium
                                                                                                                                                                                                              WO200037493-A2
                                                                                                                                                                                                                                                                         21-DE(:-1999;
                                                                                                                                                                                                                                                                                                       21-DEC-1998;
                                                                                                                                                                                                                                            29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                       Key
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Sequence including 2,5-diketogluconic acid reductase gene and purpl35
                                                                                                                                                                                                                                                                                                                                                                      The 2,5-DKG-reductase gene is prepared by recombinant DNA techniques. 2,5-DKG-reductase is used to convert 2,5-DKG stereoselectively into 2-KLG, which is an intermediate in the production of ascorbic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :
C
                                                                                                                                                                                                                                                                       Miller JV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 18; bb 6; Length 1854;
100.08; rred. No. 16;
ive 0; Hismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1853 BP; 327 A; 645 C; 587 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                         prepd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2,5-diketogluconic acid reductase; 2,5-DKG reductase;
                                                                                                                                                                                                                                                                       Lazarus RA,
                                                                                                                                                                                                                                                                                                                      New pure 2,5 di:kvto-gluconic acid reductase - precombinant DNA methods for ascorbic acid prodn.
                                                                                        /*tag= d
/!abel- 2,5-DKG-reductase gene
                    coli trp promoter
                                                 coli trp promoter
                                                                                                                                                                                                                                                                       Rasteter WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
229..234
/*Lag~ a
                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium sp. ATCC 31090
                                                                                                                                                                             84US~0620585.
83US~0508409.
83US~0508410.
83US~0508628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAN90631 standard; DNA; 1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84US-0620651.
                                                                                                                                                          84EP-0304277
         /*tag= a
/!abel= E.
252..257
                                     /*tag= b
/!abel- E.
279..283
                                                                   /*tag- c
296..1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                     Estell DA, Light DR,
                                                                                                                                                                                                                                                   (GETH ) GENEN'FECH INC
                                                                                                                                                                                                                                                                                         WPI; 1985-026535/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   P-PSDB; AAP50247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        control regions.
                                                                                                                                                                                                28-JUN-1983;
28-JUN-1983;
14-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1990
                                                                                                                                                          25-JUN-1984;
                                                                                                                                                                              14-JUN-1984;
28-JUN-1983;
                                                                                                                                                                                                                               14-JUN-1984;
                                                                                                                                         30-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                    (vitamin C)
                                                                                                                   EP132308-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN90631;
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promoter
                             promoter
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                                                           RBS
                                                                             CDS
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2 Polynucleotides (AAT72684 and AAT72685) represent 2 distinct clusters of genes encoding enzymes (AAW19734-36 and AAW19737-42) involved in sugar biosynthesis and attachment in Saccharopolyspora erythraea. The eryB genes are involved in the biosynthesis of L-mycarose and the eryC genes involved in the biosynthesis of D-desosamine. Wovel glycosylation-modified polyketides are produced by selectively altering, inactivating or augmenting these eryB and/or eryC genes and introducing them into polyketide-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene cluster; bacterium; enzyme; macrolide; antiblotic; erythromycin; secondary metabolite; eryBII; eryCIII; eryCIII; hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes involved in sugar biosynthesis and attachment – used 1
generate polyketide antimicrobials etc. with altered pattern of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.0%; Score 18; DB 18; Length 8051; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.erythraea erythromycin-synthesis gene cluster eryAI-eryK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8051 BP; 1225 A; 2898 C; 2765 G; 1163 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             Summers RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                             Staver MJ,
                                        /*tag= c
/label= eryCVI
3214..4677
                                                                                 /*Lag- d
/label- eryBVI
4674..5879
                                                                                                                         /*tag= e
/label= eryClV
5917..7386
                                                                                                                                                                                                            /*tag= g
/label= eryBVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 4B; 85pp; English.
b
eryBV
                                                                                                                                                                   /*tag~ f
/lubel- eryCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX25774 standard; cDNA; 8160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US20238
/*tag= b
/label= ery
2348..3061
                                                                                                                                                                                                                                                                                                                                     950S-0576626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                             7415..7996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Donadio S, Katz L,
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-351066/32.
P-PSDB; AAW19737-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                  (ABBO ) ABBOTT LAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycosylation
                                                                                                                                                                                                                                                                                                                                     21-DEC-1995;
                                                                                                                                                                                                                                                     WO9723630-A2
                                                                                                                                                                                                                                                                                                           23-DEC-1996;
                                                                                                                                                                                                                                                                               03-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                    CDS
                                                                                                                                                      CDS
                                                                                                                                                                                               COS
                           CDS
                                                                                                             CDS
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염
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The enzyme encoded by the sequence, 2-KLG reductase is used to convert 2,5-DKG into 2-KLG, a precursor of ascorbic acid.
See also AAN94347 and AAN94348.
                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant prodn. of 2,5-diketogluconic acid reductase - useful for converting 2,5-DKG stereoselectively into 2-ketogluconic acid, a precursor of vitamin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyketide, glycosylation, eryBIV; eryBV; eryCVI; eryBVI; eryCIV; eryBVII; L-mycarose; D-desosamine; antimicrobial; antibiotic; antifungal; fungicide; anticancer; cytostatic; anthelmintic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                  Miller JV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 1853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1853 BP; 327 A; 644 C; 588 G; 294 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                    Rastetter WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
0
/label=E. coli Trp promoter
252..257
                                          promoter
                                                                                              /*tag= d
/product=2,5-DKG reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.0%; Score 18;
00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                    Lazarus RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                          /*tag= b
/label=E.coli Trp
279..282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; fig 4; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugar biosynthesis gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
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/label= eryBIV
1048..2295
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                                                                                                                                                                                                                      83US-0508628.
83US-0508409.
83US-0508410.
84US-0620651.
84US-0620652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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                                                                                                                                                                                               87EP-0202624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 cgacctcaccgacaccga 194
                                                                    /*tag= c
296..1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match ...
Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997 (first entry)
             ..257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80..1048
                                                                                                                                                                                                                                                                                                                                                  Light DR, Estell DA,
                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-069875/10.
                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAP94624
                                                                                                                                                                                                                        28-JUN-1983;
28-JUN-1983;
28-JUN-1983;
14-JUN-1984;
14-JUN-1984;
14-JUN-1984;
                                                                                                                                                                                               01-JAN-1987;
                                                                                                                                                                   08-MAR-1989
                                                                                 mat_peptide
                                                                                                                                       EP305608-A.
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                promoter
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                                                        RBS
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AAA64890;
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                                                                                                                                                       RESULT
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88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the eryAl-eryK gene cluster from the Gram-positive bacterium Saccharopolyspora erythraea which encodes enzymes involved in the production of the macrolide antibiotic erythromycin as a secondary metabolite. The erythromycin gene cluster spans approximately 53 kb and contains at least 20 open reading frames (ORF). This sequence contains the eryBlV, eryBV, eryCVI, eryBVI, eryBVI, eryBVI, eryBVI, eryBVII genes encoding ORFs 13, 14, 15, 16, 17, 18 and 19 respectively. A DNA representing the eryG-eryAIII region of the same
                                                                                                                                                                                    /gene= "eryBVI"
/product= "dTDP-4-keto-L-6-deoxyhexose-2,3-dehydratase"
1837..6042
                                                                                                                                       /gene= "eryBVII"
/product= "dTDP-4-keto-D-6-deoxyhexose-3,5-epimerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW99389, AAW99390, AAW99391, AAW99392, AAW99393, AAW99394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences encoding enzymes involved in macrolide biosynthesis - useful for producing hybrid secondary metabolites, particularly erythromycin analogues
                                                                                                                                                                                                                                                                          /gene= "erycv"
/gene= "erycv"
/product= "dTDP-D-4,6-dideoxyhexose-3,4-reductase"
                                                                   gene= "eryBIV"
product= "dTDP-keto-L-6-deoxyhexose-4-reductase"
                                                                                                                                                                                                                        /gene="eryCIV"
/gene="eryCIV"
/product="dTDP-D-6-deoxyhexose-3,4-dehydratase"
/080..7549
                                                                                                                                                                                                                                                                                                                                                                                                                                  Raynal MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Salas JA;
                                                                                                          /dene= "eryBV"
/product= "mycarosyltransferase"
2510..323
                                                                                                                                                                                                                                                                                                                                                                                                                                 isser S, Leadlay P, Michel JM,
Fromentin C, Mendez C, Salas J
glycosylation; macrolactone; oleandomycin; ds.
                                   Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    (HMRI ) HOECHST MARION ROUSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 3; 221pp; French.
                                                                                                                                                                                                                                                             /*tag= f
/label= ORF18
                                                                                                                                                                                                                                                                                                          /label= ORF19
                                                                                                                                                                                   label= ORF16
                                                                                                                                                                                                                  /*tag= e
/label= ORF17
                                                    '*tag= a
'label= ORF13
                                                                                                  /label= ORF14
                                                                                                                                                                                                                                                                                                                                                                                            98FR-0007411.
                                                                                                                                                                                                                                                                                                                                                                             98WO-FR01593
                   Saccharopolyspora erythraea
                                                                                                                                                                   ..4840
                                                                                                                                                                                                                                                   ..7549
                                                                                                                                                                                                                                                                                            578..8159
                                                                                  210..2457
                                                                           product=
                                                                                            /*tag=
                                                                                                                                     *tag=
                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaisser S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-142938/12
                                                                                                                                                                                                                                                                                                                                                                                                                                            Salah-Bey K,
                                                                                                                                                                                                                                                                                                                                             W09905283-A2
                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                              12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                              04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cortes J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW99395.
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                                                                                                                                                                                                                                                                                              CDS
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cluster is shown in AAX25772. The genes are used to produce hybrid secondary metabolites in S.erythraea, i.e. erythromycin analogues which may have improved properties or as hybridisation probes for isolating homologous genes involved in glycosylation of macrolactones in macrolide-producing strains (specifically oleandomycin-producing strains of Streptomyces antibioticus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial infection; anti-bacterial; vaccine; whooping cough; type III secretion system; virulence factor; pathogenicity island; ss.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                4.0%; Score 18; DB 20; Length 8160;
100.0%; Pred. No. 15;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella pertussis pathogenicity island coding sequence.
                                                                                                                                       Sequence 8160 BP; 1259 A; 2927 C; 2789 G; 1185 T; 0 other;
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/product= "Protein # 1 (AAB14147)"
complement (2055..3590)
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complement (11906..13003)
/*tag= m
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complement (11532..11909)
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complement (10752..11120)
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complement (8656 ..10755)
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100.0%; Priv
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                                                                                                                                                                                                                           Best_Local Similarity
Matches 18; Conserv
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P.PSDB: AABI4111, AAB14112, AAB14113, AAB14114, AAB14115, AAB14116, AAB14117, AAB14118, AAB14119, AAB14121, AAB14122, AAB14123, AAB14123, AAB14129, AAB14129, AAB14129, AAB14130, AAB14131, AAB14132, AAB14132, AAB14133, AAB14134, AAB14135, AAB14135, AAB14136, AAB14137, AAB14137, AAB14136, AAB14137, AAB14137, AAB14137, AAB14138, AAB14140, AAB1414141, AAB14142, AAB14143, AAB141416, AAB14147, AAB14149, AAB14151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella pertussis possesses a type III secretion system. Type III secretion systems allow bacteria to target virulence factors directly at bost cells. A pathogenicity island is a compact, distinct genetic unit carrying virulence genes. The present sequence is a pathogenicity island from B. pertussis. The present sequence encodes a number of proteins involved in the type III secretion system of B. pertussis i.e. Bordetella pathogenicity protein. The proteins encoded by the present sequence may be used to treat or diagnose B. pertussis infection, e.g. as a vaccine. Mhooping couch is a disease caused by infection by B. pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides derived from Mordetella pertussis, useful for treating and diagnosing Bordetella infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 18; DH 21; Length 35026; 100.0%; Pred. No. 13;
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complement (31773..33005)
                                                              am
:t= "Orf14 (AAB14145)"
                                                                                                                           /product= "Orf15 (AAB14146)"
complement (33002..34852)
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                                                                              /product= "Or
32370..33014
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                                                                                                                                                                                                                                                                                                          98СВ-0028217.
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Matches 18; Conservative
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Ouery Match
Best Local Similarity 100.0%; Score 18; DB 22; Length 349980;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0;
Oy 214 traccocquagacaccagc 231
Db 201596 tcaccctgagacacagc 201613

0;

Gaps

Search completed: April 3, 2002, 02:03:22 Job time: 3311 sec

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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
Sequence 63, Appl
Sequence 35, Appl
Sequence 35, Appl
Palent No. 5240849
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 45,
Sequence 36,
Sequence 13,
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Sequence 13,
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Pred. No. 1.2e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30,727
FR: 19603/185 (D-1485B)
              PCT-US91_06234A-5
US-08-646-590B-35
US-08-412-184-35
5240849-4
US-09-114-541-3
US-08-396-479B-3
US-08-396-479B-3
US-08-124-981A-1
US-09-037-192-45
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US-09-037-192-45
US-09-037-193-45
US-09-037-192-45
US-09-037-192-45
US-09-037-192-45
US-09-037-192-45
US-09-037-192-45
US-09-038-1345
US-08-588-98-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.9%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: DNA (genomic) US-08-464-052-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                              2853
3647
3647
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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Best Local Similarity
   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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Sequence 1, Appli
Sequence 2, Appli
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1144.134 Million cell updates/sec
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Sequence 18,
Sequence 15,
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Sequence 1
Sequence 1
Sequence 2
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                                                                                                          April 3, 2002, 00:40:06; Search time 89.67 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-103-840A-1

US-09-103-840A-1

US-08-57-62-4

US-08-081-072-18

US-08-081-072-18

US-08-081-072-15

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US-08-551-56-5

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US-08-551-687-5

US-08-51-88-8

US-08-941-936-1

US-08-118-388-8

US-08-118-388-8
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US-08-689-411-5
US-08-689-411-5
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US-08-461-002-1
US-08-9411-1
US-08-99-411-1
US-08-99-411-1
US-08-390-878-18
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                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                 Gapop 60.0 , Gapext 60.0
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seq length: 200000000
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Match Length
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Maximum DB
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                                                                                                                  Run on:
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Sequence 5, Application US/08461002
Patent No. 614543
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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338 acgaccacaccccggtcatcgaccacccccgatgcggccgccatcgaccgcgacacc 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELEPAN: (716) 263-1304
TELEPAN: (716) 263-1300
TELEPAN: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 Dasse pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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38.9%; Score 176; DB
Best Local Similarity 100.0%; Pred. No. 1.2
Matches 176; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A. ZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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US-08-461-002-5
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APPLICANT: Chong, Pele
TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SAGUENCES: 14
CORRESPONDENCE ANDESS: 1
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
                                                                                                                              dinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NIDMER: 30,727
REFERENCE/DOCKET NUMBER: 1963/187
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (716) 263-1304
TELEFAX: (716) 263-1304
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/689,411
FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6008201
Riley M.D., Lee W.
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                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                              STREET: Clinton
CITY: Rochester
STATE: New York
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Best Local Similarity
Matches 176; Conserv
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ZIP: 14603
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ZIP: 14603
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(716) 263-1600
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                                                            LENGTH:
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TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.9%; Score 176; DB 3; 1
100.0%; Pred. No. 1.1e-74;
tive 0; Mismatches 0;
                                                                                                                                                                  NAME: GOLDMAN, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERNEC/POCKET NUMBER: 19603/186 (D-1485H)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ...ureSSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTY: U.S.A.
                                                                                           APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08461002 Patent No. 6214543 GENERAL IMPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                      ATTOKNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                               FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                               unknown
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OPERATING SYSTEM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-464-052-1
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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Fele
TITLE OF INVENTION: DAM MOLECULE FRAGMENTS ENCODING FOR
TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                348 acqaecararecryateateqarareacreergatqeqqeeqeeateqaecqeqaraere 397
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                                                                                                                                                                                                                    Length 1535;
                                                                                                                                                                                                                                                             0; Indels
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STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: Faterth Release #1.0, Version #1.30 CURRENT APPLICATION DAIA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                38.9%; Score 176; DB 4; 100.0%; Prod. No. 1.1e-74; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Flappy disk
COMPUTER: HM 10° COMpatible
OPERATING SYSTEM: PC DOSZMS DOS
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REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                        TOPOLOGY: unknown; MOLECULE TYPE; DNA (qenomic)
US-08-461-002-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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NAME: Goldman, Michael L
                                        1535 base pairs
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INFORMATION FOR SEQ 1D NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             Matches 176; Conservative
                                                                                        double
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                                                             TYPE: nucleic acid
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DB 4; Length 1535;

38.9%; Score 176;

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ZIP: 94105
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                                                 US-08-390-878-18
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                                                                                       1106 GGGGGCCACCTTTGAAGCCGTGCTAGCCAAACTGGCCGCCCCCGGGCGCGACCAACCCCG 1165
                                                                                                                                        1166 ACGACCACACCGGGTCATCGACACCCCCGATGGGGCCCCATCGACCGCACACCC 1225
                                                         278 cgcgggccacctttgaagccgtgctagccaaactggccgccccggcggcgaccaacccg 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 acgaccacacccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 cgcgggccacctttgaagccgtgctagccaaactggccgcccccggcgcgaccaacccg 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc 397
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                              PCT-US94-09863-1

Sequence 1, Application PC/TUS9409863

GENERAL INFORMATION:

APPLICANT: Riley, Lee W.

TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR

TITLE OF INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
             Pred. No. 1.1e-74; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.9%; Score 176; DB 5; 1 100.0%; Pred. No. 1.1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMNUNICATION INFORMATION:
TELEPHONE: (716,263-1000
TELEFAX: (716)-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, v.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy-disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Micha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1535 base pairs
          Best Local Similarity 100.
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 38.9%
Best Local Similarity 100.0
Matches 176; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Clinton
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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278 eqeygaccacet II haaqeeq Fet haterbaactgqcegeecccggggggaccaacceg 337 FILLI HILLI 
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APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: HITE, Owen R.

APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UUBERCULUSIS

FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08390878
Patent No. 5700683
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 176; DB 1; Length 12412;
Pred. No. 9.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
38.9%: Score 176; DB
Best Local Similarity 100.0%; Pred. No. 9.5
Matches 176; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38,498
FR: 15371A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 18:
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TYPE: nucleic acid
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ATTORNEY/AGENT INFURMATION:
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                                                                                                                                                                                                                                   TITLE OF INVENTION: VIEW NUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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Best Local Similarity
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Patent No. 5998194
GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                       Db 1789181 CGCGGGCCACCTTTGAAGCCGTGCTACCCAAACTGGCCGCCCCCGGCGCGCACCAACCCCG 1789122
                                                                                                                                                                                                                                                                                                                                                                                                                Db 1789121 ACGACCACACCCCGGTCATCGACACCCCCCGATGCGGCCGCCCATCGACCGCGACACCC 1789062
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| Patent No. 6294328
| General Information:
| APPLICANT: IELESCHHAM, Robert D.
| APPLICANT: FERSER, Claire M.
| APPLICANT: VENTER, John C.
| TILLE OF INVENTION: TUBERCULOSIS
| FILE REFERENCE: 24366-20007.00
| CURRENT APPLICATION NUMBER: US/09/103,840A
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 1
| LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 cgcgggccacctttgaagccgtgctagccaaactggccgccccggcggcgaccaacccg 337
                                                                                                                                                                                                                                                                                                                                                                                             338 acgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccqcgacaccc 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%; Score 176; DB 4; Length 4411529; 100.0%; Pred. No. 5.8e-75; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
1.2;
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILIN: DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 4411529
                                                                                                                 TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA COMPACTION TUDERCULOSIS COMPANISM: MYCOBACTERIUM TUDERCULOSIS US-09-103-840A-1
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US-08-576-626A-2
: Sequence 2, Application US/08576626A
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Best Local Similarity 100.
Matches 176; Conservative
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US-09-103-840A-1
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Sequence 4, Application US/07982712

Patent No. 5436391

GENERAL INFORMATION:

PAPLICANT: Hideya FUJIMOTO, Kimiko ITOH

APPLICANT: MiKihiro YAMAMOTO, and Ko SHIMAMOTO

TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous

TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
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           APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: DONADIO, S.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
TITLE OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diskette, 3.50 inch, 144 mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 938-3137
TELEPHONE: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASLSKU VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
                                                                                                                                                                                     E: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CONTACTOR OPERATING SYSTEM: DOS SOFTWARE: FastSKQ Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5311 ACGACGGGCHGCTGGCG 5328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCEPTED TO THE STATE OF TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MODIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dianne Casuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                            STREET: 100 Abbott
CITY: Abbott Park
STATE: 111inois
INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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3.8%; Scor.
100.0%; Pre
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                                                                                                         231 caatacgacggcatgtc 247
                                                                                                                              358 CAATACGACGGCATGTC 374
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TYPE: nucleic acid
                Query Match 3.8'
Best Local Similarity 100.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109-4280
                                                                                                                                                                                                                  RESULT 14
US-08-449-093A-18
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Patent No. 5641654

GENERAL INFORMATION:
APPLICANT: No. 5641654oru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: No. 5641654oru MAKI, Kenjiro YAMAGUCHI, Ayumi
APPLICANT: No. 5641654oru MAKI, Kenjiro YAMAGUCHI, Ayumi
TITLE OF INVENTION: NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diske, Bronstein, Roberts & Cushman
SIREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.8%; Score 17; DB 1; Length 42; Best Local Similarity 100.0%; Pred. No. 28; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-4280
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk,3.50inch,1.4Mb storage COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COPERATING SYSTEM: Macintosh Classic
SOFTWARE: Macrosoft Word Version 4.0A
CURRENT APPLICATION DATA:
                OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/982,712
FILING DATE: 19921127
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/081,072
FILING DATE: June 22, 1993
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA to genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-07-982-712-4
                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 gactggctacaccccga. 173
                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 742 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 GACTGGCTACACCCCGA 23
                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 42 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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CITY: Boston
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Seel Local Similarity 100.0%; Score 17; DB 1; Length 742; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0; All Conservative 0; Mismatches 0; Indels 0; Gaps 0; All Conservative 0; Mismatches 0; Indels 0; Gaps 0; All Conservative 0; Mismatches 0; Indels 0; Gaps 0; All Conservative 0; Mismatches 0; Indels 0; Gaps 0; All Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps
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Query Match
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: DIAGNOSIS

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
COUNTRY: Boston
STATE: Boston
STATE: Macantestts
COUNTRY: USA
ZIP: O2109-4280
COMPUTER: REDABLE FORM:
MEDIUM TYPE: Floppy Disk,3.50inch,1.4Mb storage
COUNTRY: Apple Macintosh
COMPUTER: Apple Macintosh
COM
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Search completed: April 3, 2002, 03:06:30 Job time: 8784 sec

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Gaps ;

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AAA41556 LD25748.5
AQ330146 hbxb0046H
AAA4032 LD15267.5
AL171364 Tetraodon
B10564 F1984-T7 IG
AQ55308 nbxb0063H
BEB50262 uw15a09.y
BFB60432 HwHCU370_B
BE490643 WHEU370_B
BC490643 WHEU370_B
BC50060 RH122_58_AW076994 F103c02.y
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AQ38116 mbxb00053
AA54704 nt60407.s
BE270509 601185491
AA174323 AA174323
BG59443.2 MAJFV1_1
BC69943.2 GO2679121
BF568065 HV_CEa001
BE196478 HVSMEND09
AL171161 Tetraodon
BF026228 601672803
AL301470 Tetraodon
BH132519 ENTN 10941
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: DCTDOTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

Http://image.llnl.gov

plate: LLAM10467 row: d column: 21

High quality Sequence stop: 739.

Ince Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG285414 1100 bp mRNA EST 21-FEB-2001
602409782F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4539236 5',
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/ Organism="Homo sapiens"
/ db_xref="taxon:9606"
/ clone="IMAGE:4539236"
/ tissue_type="adenocarcinoma, cell line"
/ lab_host="DH10B (phage-resistant)"
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BGB10322
AQ848738
BGG99432
BF268065
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BFO26228
CNSO4PLX
BH132519
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CNSO1IWW
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AQ398116
AA654704
BE270509
B1168066
AA941556
AQ330146
AA440332
CNS01X7V
B10564
AQ365308
BE850262
BF804832
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BF083249
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mRNA sequence.
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TITLE
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COMMENT
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KEYWORDS
SOURCE
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BG285414
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BF202807 WHEI784_H
BF924284 FC.NT022
AQ573457 nbxb0081E
AW287746 LCI_271_H
BE499331 WHE0973_F
BE490055 WHE0364_A
BE416425 WIG008.E1
AA94237 LD28056.5
BI164231 KE0433.5
A1518445 LD28056.5
                                                                                                                                               April 2, 2002, 22:46:21; Search time 1557.61 Seconds (without alignments) 3125.197 Million cell updates/sec
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                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
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AW287746
BE499331
BE490055
BE416425
BE416426
AA949237
BI164631
AI518445
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BF202807
                                                                                                                 nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Minimum DB seq Maximum DB seq

Maximum

Word size

Searched:

Database :

Perfect score:

Sequence:

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Run on:

Scoring table:

Score

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Result

119 119 119 119 119

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HV_CEA001 HVSMEh009 Tetraodon 601672803 ENTN109TR 602110941 Anopheles AL534377

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Gaps

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Indels

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Mismatches

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Pred.

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Best Local Similarity 100.
Matches 19; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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MEDLI NE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                          RESULT
BF924284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: Xhoī; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total kNA, and poly(A) RNA were prepared, a cDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." 3 others
                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF202807 454 bp mRNA EST 06-NOV-2000 WHEI784_H02_0042S Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHEI784_H02_004, mRNA sequence.
BF202807.1 GI:11117549
                                                                                                                                                                                                                                                                                                                                                                                                 Caps
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
for primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .454
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/organism="Triticum destivum"
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/clone="WHE1784_H02_004"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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DB 11; Length 454;

4.2%; Score 19;

Query Match

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Another "orders netrons, tumos; vector; puch8; Site_1: Smal; Site_2: Smal; A mini library was made by cloning products derived from tokestess Per (U.S. betters Patent application by 196,716 - ludwing institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., ad Sllvaw, Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.K., Reis, L.F., de Souza, S.J. and Simpson, A.J. saures, F., and the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: dsimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seven in the following URL
(http://www.ludwig.org.br/scripts/gethimi2.pl?tl-RC2&L2-RC2-NT0225-271100-011-h09&t3-2000-11-27&t4*1)
Seq prime: puc IR forward
                                                                                                                                                          БF924264 458 bp mkNA EST 19-JAN-2001
RC2-NT0225-271100-011-h09 NT0225 Homo sapiens CDNA, mRNA sequence.
BF9242844
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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69;
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Zib xret "taxon:9606"
Zetone lib "Nicaes"
Zev stage "Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 40 High quality sequence stop: 90.
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                                                                                                                                                                                                                                                           BF924284.1 G1:12320172
Mammalia, Eutheria;
1 (bases 1 to 458)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 c
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Best Local Similarity 100.
Matches 19; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

DEFINITION

ACCESSION

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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
1 (bases I to 525)
Anderson, O. D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes: Pre-anthesis spike cDNA library
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific Wost Area, Western Regional Research Center
800 Buchanum Street, Albany, CA 94710, USA
Tel: 510559573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorghum bicolor
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Spermalophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.

( pases 1 to 494)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.
An ESY database from Sorghum: light-grown seedlings
Unpublished (2000)
On Jan 6, 2000 this sequence version replaced gi:6677590.
Contact: Cordonnier-Pratt, MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmprattenga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below phird quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHEO9741 529 bp mkNA EST 04-AUG-2000 WHEO974_FOR LISZS Wheat pro authesis spike cDNA library Triticum aestivum cDNA clone WHEO974_FO8_LD15, mkNA sequence.
                                                                                                                                                                                                                                                                                                                                                            The University of Georgia
Plant Sciences Hullding, km. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 10; Length 494;
Pred. No. 69;
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High quality sequence stop: 401
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                GI:6859737
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Best Local Similarity 100.
Matches 19; Conservative
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                AW287746.2
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COMMENT
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                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                AUTHORS
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/clultivar="Nipponbae"
/db_xref="taxon:4530"
/clone="nbx0081E24r"
/clone_"lbb="CuGis Rice BAC Library"
/clone_"lbb="CuGis Rice BAC Library"
/clone_"lbb="CuGis Rice BAC Library"
/clone_"lbb="CuGis Rice BAC Library"
/clone_"lbb="cucis One of two most popular grains in the world Half of the world popular grains in the world Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledomous rice is a diploid plant (2n-24) with a happioid genome equivalent of 4% bpp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of 4% bpp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of architect positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare aricity. The library contains 36,864 clones with an average insert size of 1285. Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Two high density litters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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LG1_271_H06.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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AQS73457 477 bp DNA GSS 02-JUN-1999 nbxb0081EZ4r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0081EZ4r, DNA sequence.
                                                                                                                                                                                                                                                                                                             1 (bases 1 to 477)
Wing, R.A. and Dean, R.A.
Who BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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100.0%; Pred. No. 69;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 428.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Japonica"
                                                                                                                            AQ573457.1 GI:4973546
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Matches 19; Conserv
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AW287746
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source

FEATURES

Query Match

DEFINITION AW287746/C

RESULT

QQ

ACCESSION

BASE COUNT ORIGIN

ö

Gaps

.,

us-09-785-904-2.olig.rst

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales: Pouceae; Pooldeae; Triticae; Triticam.

1 Triticae; Triticam.

2 Triticae; Triticam.

3 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fonton,R.D., Han P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Saton,C.L. and Tong,JC.

The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling cDNA library

LU Unpublished (2000)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA

Fax: 5105595773

Fax: 5105595773
                                                                                                                                                                                           /crganism="Triticum aestivum"
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/note="Vector: Lambda Uni ZAP XR, excised phagemid;
/note="Vector: Lambda Uni ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a CDNA library was made, and the CDNA clones were in vivo excised to give phluescript phagemids in the TJ close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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Fax: 5105595818
Email: oandersn@pw.usda.gov
Se.juence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Fritceae; Tritcom.

1. (bases 1 to 575)

2. Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier; S., Dubcovsky, J., Feuillet, C., Cale, M., Graner, A., Gustafson, P., Hermann, R.G., Holton, T., Jacquemin, J.M., Jian, J., Joudrier, P., Lanquide, P., Laroo, C.R., Lin, J.J., McGuire, P., Ogihara, Y., Perchioni, N., Qualset, C., Schuch, M., Selvaraj, G., Sharillou, M., Sorrella, M., Warbuston, M. and Wenzel, G.

Expressed Sequence Tags for Species of the Triticeae

M. Unpublished (2000)
                                                                       /tissue_ivpe="Seeding" |
/tissue_ivpe="Seeding" |
/dev_stage="Five-day old seedling" |
/dev_stage="Five-day old seedling" |
/dev_stage="Five-day old seedling" |
/dev_stage="Five-day old seedling" |
/dev_stage="Seeding" |
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/cultivar="Norin 26"
/db_xref="Laxon:4565"
/clone="MuG008 E09"
/clone="MuG008 E09"
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/clone="lib="TEC MUG Wheat Spikelet"
/clone=lib="TEC MUG Wheat Spikelet"
/clone="lib="TEC MUG Wheat Spikelets"
/clone="reckes" scale 6-7"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; M13 Reverse sequencing primer used. 1.2 Kbp average
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MUG008.E09R990628 ITEC MUG Wheat Spikelet Library Triticum aestivum
CDNA clone MUG008.E09, mRNA sequence.
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Contact: Ogihara Y
Kihara Institute for Biological Research, Yokohama City University
Manoka-cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
Tel: 81 45 820 1903
Fax: 81 45 820 1901
/clone="WHE0364_A04_A08"
/clone_lib="Wheat cold-stressed seedling cDNA library"
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International Triticeae EST Cooperative (ITEC)
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100.0%; Pred. No. 69;
Live 0; Mismatches
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AUTHORS

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FEATURES

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Eukaryota: Metazoa: Arthropoda: Tracheata; Hexapoda; Insecta; Pterygota; Mooptera; Endopterygota: Diptera; Brachycera; Puscomorpha; Ephydroldea; Drosophilidae; Drosophila.

1 (bases 1 to 598)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /noie="Organ: embryo; Vector: pOT2; Site_1: EcoR1; Site_2: Xhoi; Sized Iractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RE0444 (Sprime RE Drosophila melanogaster normalized Embryo PFlc-1 Drosophila melanogaster cDNA clone RE04443 5 similar to CG452: PB10004532 located on: X 6D1-6D2;: 04/11/2001, mRNA sequence.
                                                                                                              fruit fly.

Buchosophila melanogaster

Eukaryota: Mctazoa: Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryyota: Neoptera: Endopteryyota: Diptera: Brachycera;

Muscomorpha: Ephydroidea; Drosophilae: Drosophila.

1 (bases 1 to 583)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsanq, G.,
LD28056.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD28056 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab one Cyclotron Rd, Berkeley, CA 94720, USA Pax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 280 row: E column: 8 Plate: 280 row: E column: 8 High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="LD28056"
/clone_lib-"LD Brosophila melanogaster embryo pOT2"
/clone_lib-"LD frosophila melanogaster embryo pOT2"
/clone_lib-"LD frosophila melanogaster embryonic"
/dev_stage="0" to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
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69;
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/ordanism-"Drosophila melanogaster"
/db_xref-"taxon:7227"
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BDGP/HHM! Drosophila EST Project
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Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Owalset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warbutron, M. and Wenzel, G.
International Triticeae Est Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

LD Onpublished (2000)
Contact: Ogihara Y
Kihara Institute for Biological Research, Yokohama City University Maioka cho 641-12, Totsuka-ku, Yokohama 244-0813, JAPAN
Tel: 81 45 820 1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_1: EcoRI; Site_2:
pr used: 1.2 Kbp average
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                                                                                                                                                                                                                                                                                                                                                       BE416426 581 bp mRNA EST 24-JUL-2000 MUG008.E10R990628 ITEC MUG Wheat Spikelet Library Triticum aestivum cDNA clone MUG008.E10, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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                                                                                                                                                                  Caps
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/tissue_type="Young spikelets"
/dev_stage="Feekes' scale 6-7"
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69;
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XhoI; M13 Reverse sequencing primer used.
insert size."
199 c 167 g 82 t 6 others
                                                                                                                          10; Length 575
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                                          4 others
                                                                                                                                                                  0; Indels
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International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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/organism="friticum aestivum"
/cultivar="Norin 26"
/db_xref="taxon:4565"
/clone="MUG08.E10"
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69;
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100.0%; Pred. No.
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Pred. No.
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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BE416426.1 GI:9414272
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                        ert size."
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RESULT 10 AA949237 LOCUS

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BASE COUNT ORIGIN

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/dev_stage="0-24 hours mixed stage embryonic"
/hab_host="DHS-alpha TonA"
/note="Organ: embryo; Vector: pFlc1; Site_1: Xhol; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
a 185 c 157 g 99 t lothers
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LD37958 5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD37958 5prime, mRNA sequence.
AI518445
AI518445. GI:4424299
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera;
M.scomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 626)
Hurvey,D.; Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
                                                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003438: arm:X [6347108,6646644]
estimated-cyto:6B1-6D3: 04/11/2001
Plate: RE.43 row: D column: 7
High quality sequence stop: 490.
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One Cyclotron Rd, Berkeley, CA 94720, USA
Exa: 510 486 6798
Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
plate: 379 row: E column: 10
High quality sequence stop: 413.
Location/Qualifiers
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XLI Blue"
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                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE04343"
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/db_xref="taxon:7227"
/clone="LD37958"
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Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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69;
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Best Local Similarity 100.0
Matches 19; Conservative
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1 (bases 1 to 650)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champer,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,M., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
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                                                                                                                                                                                                                                                                                                                                                                   BI168066 650 bp mRNA EST 09-JUL-2001 RE08607.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE08607 5 similar to CG4532: FBan0004532 located on: X 6D1-6D2;: 04/11/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cloue_lib-"RE Drosophila melanogaster normalized Embryo
                                                                                                                                                  Gaps
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hit genomic AE003438; arm:x [6347108,6646644]
estimated-cyto:681-663: 04/11/2001
Plate: RE.86 row. A column: 7
High quality sequence stop: 515.
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/lab_host="DH5-alpha TonA"
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                                                                                                Length 626;
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/ordanism-"Drosophila melanogaster"
/db xrel "laxon:7227"
/clone-"REOH607"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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                                                                                           DB
70;
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Pred. No.
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100.0%; Pre
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Contact: Stapleton, M.
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                                                                                                                                                                                                                      563 CCACGACGGCTGCTGGC 581
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I (bases 1 to 701. Manual Pana, R.A. and Dean, R.A. and Dean, R.A. A. BAC End Sequencing Framework to Sequence the Rice Genome
                                                                                                                                                                                               fruit fly.

Drosophila melanogaster

Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta:

Bukaryota: Metazoa; Arthropoda; Tracheata; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 742)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
                                        AA941556 742 bp mRNA EST 23-APR-2001 LD25548.Sprime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD25748 5 similar to CG4532: FBan0004532 located on: X 6D1-6D2;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ330146 761 bp DNA GSS 08-JAN-1999 nbxb0046H15f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0046H15f, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AEO03438: arm:X [6347108,6646644]
estimated-cyto:6B1-6D3: 04/10/2001
plate: LD.257 row: D column: 12
High quality sequence stop: 605
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/db_xref="taxon:7227"
/clone="LD25748"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                     On May 1. 1998 this sequence version replaced gi:3101469.
Other_ESTS: LD25748.3prime
Contact: Stapleton, M.
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4.2%; Score 19; DB 10; Length 742;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels
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One Cyclotron Rd, Berkelny, CA 94720, USA
Fax: 510 486 6798
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                                                                                                                                         AA941556.2 GI:13767860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ330146.1 GI:4121996
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100.0%; Pred. No. 70;
Live 0; Mismatches 0; Indels
              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
                                                                                 High quality sequence stop: 359.
Location/Qualifiers
Unpublished (1998)
Contact: Wing RA
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Search completed: April 3, 2002, 01:30:31 Job time: 9850 sec

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AE00716 Mycobacte 186264 Sequence 18 AR47695 Sequence 284498 Mycobacterize 295584 Mycobacterize AE007053 Mycobacterize AE007058 Mycobacterize 295585 Mycobacterize AL583920 Mycobacterize AL583929 Mycobacterize AL5839569 Mycobacterize AL583959 Mycobacterize AL58565 Treptomy AC046159 Homo sapitational AF275943 Streptomy AC046159 Homo sapitational AC075075 Streptomy AC076889 Sequence
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AE006921 Mycobacte
AE007028 Mycobacte
AE077028 Mycobacteri
AR14764 Sequence
29558 Mycobacteri
274410 Mycobacteri
295390 Mycobacteri
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Unpublished
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Continuation (4 of
AC025052 Homo sapi
AC023210 Homo sapi
AL111680 BOLFYLIS
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AC023212 Homo s
AC021263 Homo s
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AC084064 B
AC087228 B
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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AE006995
MTCN22C8
MLCB1779
MLEPRIN3
MLEPRIN3
AB032367
AC046159
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MTCY251
MTY13E12
AE007160
186264
AR06715
AR147696
AE007053
MTCX9F9
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MSGY348
AE007036
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AE007028
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AB032367
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AC084064
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2510.033 Million cell updates/sec
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                                                                        April 2, 2002, 22:44:13 ; Search time 2977.34 Seconds
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Post-processing:

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98.98;
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/db_xref="G1:2326949"
/db_xref="G1:23
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LDVRQVNCSVSSAGVLRGLHFAQLPPSQAKYVTCVSGSVFDVVVDIRECSPTFGRWDS
VLLDDQDRNIYVSDGLAHGFLALQDNSTVMYLCSAEVNPQROHTICATDPTLASIRRW
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Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
705-035, South Korea
3 (bases 1 to 3453)
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Direct Submission
Submitted (14-AUG-1997) Tae-Yoon Lee, Microbiology, College of Submitted (14-AUG-1997) Tae-Yoon Lee, Microbiology, College of Submitted (14-AUG-1997) Tae-Yoon Lee, Microbiology, Namku, Tae Medicine, Yeungamam University, 317-1, Daemyungdong, Namku, Tae Medicine, Yeungamam University, 317-1, Daemyungdong, Namku, Tae Sequence update by submitter on Aug 14, 1997 this sequence version replaced gi:1304703.
On Aug 14, 1997 this sequence version replaced gi:1304703.

I cocation/Qualifiers
I cocation/Qualifiers

//Clone="Pissing" August 1773" 
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/protein_id="AAB66649.1"
/db_xref="G1:2326951"
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Length 3453;

DB 1;

Score 415.8;

91.88;

Query Match

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Mahairas,G.G., Subo,P.J., Hickey,M.J., Singh,D.C. and Stover,C.K. Molecular analysis of genetic differences between Mycobacterium boyes HCG and virulent M. Lewis 5.
J. Barteriol. 178 (5), 1274-1282 (1996)
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Mahairas G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and Stover, C.K. Direct Submission

Direct Submission

Submitted (29-AUG-1995) Mark J. Hickey, Molecular Microbiology, PathoGenesis Corp., 201 Elliott Ave. W., Seattle, WA 98119, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /note="site of deletion breakpoint in this organism. Virulent M. bovis has additional 10 kbp at this site" 637~\rm c 416~\rm g 214~\rm t
                                                                                                                                                            358
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Mycobacterium bovis BCG DNA flanking deletion region 3.
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Pred. No. 4.6e-56;
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0; Mismatches
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/db_xref="taxon:1765"
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WA 98119, USA
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/db_xref="taxon:1765"
misc_difference replace(1400. .>9281,"")
COUNT 1706 a 3191 c 2929 g 1453 t 2 others
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1 (bases 1 to 9281)
Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C. and St Molecular analysis of genetic differences between Mycobovis BCG and virulent M. Dovis GCG.
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Mahairas, G.G., Sabo, P.J., Hickey, M.J., Singh, D.C.
Direct Submission
Submitted (29-40G-1995) Mark J. Hickey, Molecular
PathoGenesis Corp., 201 Elliott Ave. W., Seattle,
Location/Qualifiers
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Conservative
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Best Local Similarity 98.0
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Actinomyvetales; Corynebacterineae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Mycobacteriaceae; Pleischman R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeRoy, R., Podson, R., Gwinn, M., Haft, D., Hickey, E., Sulzberg, S.L., Nelson, W., Unnyam, E.A., Ermolaeva, M., Sulzberg, S.L., Nelson, A., Hiter, A., Hiterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A., and Hishal, W.
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Pleischumann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischumann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Veterson, J., DeBoy, R., Bodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberd, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Direct, Submission
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Mycobacterium tuberculosis CDC1551
Bacteriu; Pirmicutes; Actinobacteria; Actinobacteridae;
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/strain="CDC1551"
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Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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Mycobacterium tuberculosis (FRC1551,
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AE006921 AE000516
AE006921.1 GI:13879142
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/note="clinical strain"
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/product = hypothetical prolein"
/product = hypothetical prolein"
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SDLAGARDSGVDFNRFYGFWVAASSARVILRLIPVLTAC"
7390
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/gene="MT0104"
/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; identified by Glimmer2; putative; conserved hypothetical protein, authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                            /noice-"similar to SP:P46840 PID:559912; identified sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         El-E2 family"
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/genew"MT0102"
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWRCIRCGDFALGGPQGRGAPEDAPIIMRGKALRQAIITRALGVERLYRALVLALAAW
AVWEPRGARGAIQATLDRDLPVLRAAGFKVDOMTVIHALEKALAAKFSTLALITGMLA
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3791.
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nucleosidase/5-adenosylhomocysteine nucleosidase,
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1449. .2123
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                                                                                                                                                                                                                                                                                                       /note="identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Bloa; similar to MTCY336.35c"
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3120, 4280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinopacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceau; Mycobacterium; Mycobacterium; Mycobacterium; Mycobacterium; Mycobacterium; Mycobacterium; Lo 10019)
1 (bases 1 to 10019)
14. S. and Jacobb, W. B. Jr.
Cloning, sequencing, and identification of Mycobacterium bovis BCG biotin biosynthetic genes by complementing two Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein
College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA
                                                                                                                 9191
                                                                                                                                                                                                                                                                                                     9190 TGGATGTGTCCACCCGCCAGGCCGCAAAGCCGACCTGGCCGGCAAAGCCGCTCAATATC 9131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tggatgtgtccacccgccaggccgccgaagccgacctgccggcaaaggc--ctcaatatc 118
                                                                                                                                                                                                                                178
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtgrtagccaaactggccgccccggcgcgaccaaccccgacgaccacaccccggtcatc 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gacaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaac 417
                                                                          1 gatcggcgagggcgcacatcaaagtgattcgcgccctttttcgcccacctgcccgccgcgg 60
                                                                                                 gtocogacgagottggcccgctacgcccagogggtcatggactggctacaccccgacggcg
                                        4 ;
Length 9764;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sub_species="BGG"

Mb_xref="taxon:33892"

complement(299...1038)

/note="ORF1; similar to MTCY336.37"
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Score 410; DB 1; I
Pred. No. 2.1e-56;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Pasteur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                smegmatis biotin mutants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis BCG. Mycobacterium bovis BCG
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90.5%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
2 (bases 1 to 10019)
                  Best_Local Sim:larity 98.0
Matches 447; Conservative
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AF041819
  Query Match
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AF041819/c
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AUTHORS
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laboratory strains
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AE007028 AE000516
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447; Conserv
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Matches 4'
                                                                 BASE COUNT
ORIGIN
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RAITGEPLAPQLTAATAORGGLIGEAHIXVIRALERPPARRGGCWHPPGRRSRPGRO
SRSISSRRAGPLRPAGGLATPRRRPHRHRTRPQTRHHPEQPAIRRHVTAKWLPDPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GELGQHNGLPVSIVVTTLTDLQTGACKGFTGGGTLLPMADVIRWTSHAHHYSPASGR
YPQAIFDHGTPLALYHTKRLASPAQRIMLFANDRGCTKPGCDAPAYHSQAHHVTGWTS
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CSLGMLTABQVDQLAARGVHRYNHNLFTARSFFANVVTTHTWEFRWOTISMVRDAGME
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VAAFRLALPRIMLRFAGGREITLGDLGAKRGILGGINAVIVGNYLFTLGRPAEADLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MIGLSATGVLVGGLWAWIAPPIHAVVAITRAGERVHEYLGSESQ
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RLRYGALDFDTVPLSRGDHALTYVTQAPPVFFARRPLQIALTLMWPAGIASLVYALLA
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7455. 18504
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/note="BioB; similar to MTCY336.15c"
                                        4957. .5466
/note="ORF6; similar to MTCY336.32c"
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/note="ORF8; similar to MTCY336.16"
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/transl_table=11
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/transl_table=11
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/translation="RWAGRDMGDFLDEPLEDILSTPEVSHVFGDTKLGSAVPTPPVLJ
VQAVHDYLIDVSDIDALADSYTAGGANVTYHRDLFSEHVSLHPLSAPWTLRWLTDRFA
VRPLTDHRVTTWPTIFNPYTAGRANVTAVIAAKVITGRKLSRRPL"
1 3134 C 3655 g 1774 t
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Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,
Peterson,J., DeBoy, W.C., Gwinn,M., Haft,D., Hickey,E.,
Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H.,
Gill,J., Mikula,A. and Bishai,W.
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Myrobacterium tuberculosis CPC1551, section 114 of 280 of the
                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                        6573 TGGATGTCCACCCGCCAGGCCGCCGAAGCCGACCTGGCCGGCAAAGCCGCTCAATATC
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                                                                                                                                 90.5%; Score 410; DB 1; Length 10019; 98.0%; Pred. No. 2.1e-56; ive 0; Mismatches 5; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTITHIHIHIHIHIHITHITHIHIHIHIHIHIHIH 6214 CACGACGCGGGCTGCCGGGCTGCTGCTGCTGCTGCTGCTGCTGGTTGATC 6179
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Mycobacterium tuberculosis (181155)
                                                     3655 g
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FEATURES

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RGATULAHNYOLPATODVADHYGDSLALSRYAARAPEDTIVEGGHFMAETAKILSPH
KTVLIPDQRAGCSLADSITPDELRAWKDEHPGAVVSYVNTAAVKALTDICCTSSNA
VDVASIDPDREVLECPDGFIGAHVRRYTGRKNLHWARGECHVHAGINGDELADOARA
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GMLHQLRRAAPEVDFRAVNDRASCKYMKMITPAALLRCLVEGADEVHVDPGIAASGRR
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GLARVIKGRAHNDEGRQLLEGOLTEMTYVAVIRMAGDFLDEPLEDILSTPEVSHY
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FGLTKLGSRAVPPPPUTYTHENTITMPTIFNPTTRENTYTAGARNTYRRDLFSSHVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to SP:P11458 GB:X12713 PID:581137 GB:U00096 PID:1651334; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTVLNRTDTLVDELTADITNTPLGYGGVDGDERWAAEIRRLAHL
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complement(5660. .6193)
/gene="MT1629"
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complement(4063. .5430)
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/transl_table=11
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6419. .7468
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SRSISSRRAGPLRPAGHGLATPRRRPHRHTRPQTRHHPEQPAIRRHVTAKWLPDPPPS
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VCCGGILGMGETLQQRAEFAARLAELCPDEVPLNFLNPRPGTPFADLEVMPVGDALKA
VAAFRLALPRTMLRFAGGREITLGDLGAKRGILGGINAVIVGNYLTTLGRPAEADLEL
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QAHHYTAWTSTGRTD1TDLTLACDPDNRLAEKGWTTHKNTHGHTEWLPPPHLDHGGPR
TNTFHHHEKLLRHNDEDNHDDP"
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
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                                                                                                               1. :1//83
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complement(831. .1499)
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3317. 3800
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                                                                                                                            LRVLHDGTAVTGLLVVRPDGGG ITSARSVILATGGGLGHLYSATTURAGGLAGGL

MAGYANYDLEFIQFHPTMLFAGRAGGRFD LITEA IRCEGALIVDRGONS ITAGVHPMG

DLARRDVVAAA IDARLKATGDPCVYLDL, RGIEGFASRFPTVASCRAAGIDPVRQOP

VVPGAHYSCGGIVTDVYGQTELLGLYAAGEVARTGLHGANRLASNSLLEGIVVGGRAG

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AR096713
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Riley, L.W. and Chong, P.
DNA molecule tragments encoding for cellular uptake of
Mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 1 01-MAY-2001;
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Riley, L.W.
DNA molecule encoding for cellular tuberculosis and uses thereof
Patent: US 6008201-A 1 28-DEC-1999;
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Bacteria; Firmicutes, Actinobacteridae;
Actinomycetales; Actinobacterineae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Aycobacterium; Mycobacterium tuberculosis complex.

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Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry 111, C.E.,
Harris, P., Badcock, R., Basham, D., Brown, D., Chillinyworth, T.,
Tekaia, F., Badcock, R., Basham, D., Brown, D., Chillinyworth, T.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quall, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B.G.
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Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced 91:2117233.
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                                                                                                                                  tggatgtgtccaccegccaggccgccgaagccgacctgccggcaaaggc--ctcaatatc 118
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                                    Gaps
                                                                   gatcggcgaggcgcacatcaaagtgattcgccctttttcgcccacctgcccgccgcgg
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                                            available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TH genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is proceeded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
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Details of M. tuberculosis sequencing at the Sanger Centre are
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/strain="H37Rv"
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/strain-"H37Rv"
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/protein_id="CAB09072.1"
/db_xref="G1:2117272"
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/gene="Rv1566c"
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/clone="Y48"
33. .32091
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/note="Rv1565c, (MT('Y2')
protein
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/gene="Rv1565c"
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Conservative
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Best Local Similarity
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                                                                        probable adenosylmethionine-8-amino-7-oxononanate aminotransferase (EC2.6.1.62) 006622. Contains aminotransferases (EC3.6.1.62) 006622. Contains aminotransferases class-III pyridoxal-phosphate attachment site (ES00660). FASTARcesults, BIOA MYCLE P4548 (436 aa) opt: 2534; E(): 0; 85.1%identityin 436 aa overlap. Also similar to other M. tuberculosis proteins e.g. MTCV227.12c, (449 aa). FASTA score: E():3.5e-16; 29.5%identity in 421 aa overlap. TBparse scoreis0.874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVTMTSWPSRLFAFTDNVCPPDACPLVPFGVNYYIYPVMMGGIG
AAATANTGEVERMLKGWYMSFWPIISIAVITVTSIAGYALAGFSERYWH"
3791. 5104
/gene="bloa"
3791...5104
/gene="bloa"
/note="Rv1568, (MTCY336.35c), bloa, len: 437. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFLAMSICOPHGGMHSLWTDVLAAQVFAPQVPRDYDNAYSAAFEAD.GARAFINAGOTION
VEPVVOGAGGMRFHDPRYLHDLRDLCRRY EVLLI FDE LATGFGKTGALFAADHAGVSP
MRCVGKALFGGYLLATGARVAHTISAGAAGAMHGBFFRANDFACAVSYASVE
LLLGQDWRRRITTETELAAGALFAGLTARALPAYTDVRVGGALGVIECDRPVDLAVATPAA
LDRGVWLRPFRNLVYAMPPYICTPAAEITQITSAMVEVARLVGSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pyridoxal-phosphate attachment site (PS00599). FASTA results, BIOF_MYCLE P45487(385 aa) opt: 1971; E(): 0; 80.1% identity in 381 aa overlap. Also similar to MTCY10H4, 32, FASTA score: E(): 5.5e-29;37.4% identity in 393 aa overlap.
                                                                                                                                                                                                                                                                                                                                                                                  /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Rv1569, (MTCY336.34c), bioF, len: 386. Function: probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-II
                                                                                                                                                                                              complement(3030. .3036)
/note="possible RBS, AAGGAGG, for Rv1566c"
complement(3258. .3263)
/note="ASNI site: ATTAAT; probably linking fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="PS00600 Aminotransferases class-III pyridoxal-phosphate attachment site" 5101. .6261
                /product="hypothetical protein Rv1566c"
/protein_id="CAB09071.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"hypothetical protein Rv1567c"
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/db_xref="G1:2117270"
/db_xref="SPTREMBL:006623"
                                                                                                                                                                                                                                                                                                                     /gene="Rv1567c"
complement(3259. .3543)
/gene="Rv1567c"
                                                                                                                                                                                                                                                                                                    complement(3259. .3543)
                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/transl_table=11
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                                                                                                                                                                               VQPPFGTARSR"
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5101. .6261
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/gene="bioF"
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/gene="bioA"
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/Lrānslalion~"MKAATQARIDDSPLAWLDAVQRQRHEAGLRRCLRPRPAVATELD
LASNDYLGLSRIPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQQFEAELAEFVGAAA
GILFSSGYTANIGAVVGLSGPGSLIJVSDARSHASLVDACRLSRARVVYTPHRDVDAVD
                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis H37Rv complete genome; segment 5/162. Z74410 AL123456 Z74410.1 GI:3261600
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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1 (bases 1 to 38380)

20le, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tggatgtgtccarccgccaggccgccgaggcgacct.gccggcaaaggc--ctcaatatc
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 2.3e-56;
                                                                                                                                                                                                                                                                                                                                                                          9
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/db_xref="G1:2117268"
/db_xref="SWISS-PROT:006621"
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/codon_start=1
/transl_table=11
/product="bioF"
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97.8%;
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gene

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available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparese (Krogh) supplemented of TB genes implemented in TBparese (Krogh) supplemented of TB genes in increase in the observed/expected third position G + C.

GAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (Atg., 9tg., or 'ttg) which is preceded by an upstream ribosome binding site sequence (Optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                  Parkhilly.

Direct Submitssion

Submitted (11-JUW-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur. 28 rue din Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:1405752.
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Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T., Connor,R., Davias,R., Devlin,K., Feltwell,T., Gentles,S., Hamlin,N., Holroyd,S., Hernsby,T., Jagels,K., Krogh,A., McLean,J., Woule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A., Safandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S., Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and Barrell,B.G.
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DLKCOLGKQOITPAGTTIVFAAAPVIVAGTTLLIAAIAPLVATGSPLDPSADLFAVVG
LLFLGTVALTLAGIDFGTSFGGMGASETITAALVEPTILLIAVFALSIPAGSANLGAL
VASTLOHPGHVVSLAGOVLAFVALVIVIVAETGRLPVDNPATHLELTWVHEAWVLEYAG
PRLALVEWAAGWRLTVLLALLANLFLPWGIAGAAPPALDVITGVVAVAAKVAILAVLLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mycobacterium tuberculosis H37Rv"
/strain="H37Rv"
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/strain="H37Rv"
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/product=hypcD
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/db_xref="G1:1405754"
/db_xref="SPTREMBL:010881"
                                                                                                                                                                                                                                                                  complete genome sequence
Nature. 393 (6685), 537-544 (1998)
98295987
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/clone="Y251"
6. .956
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967. .1629
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/gene="hycP"
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spiP7554 HIRTE_ECOLI HYDROGENAST 4 COMPORET E (216
28.5.54 identity in 216 as overlap** COMPORET E (216
25.54 identity in 216 as overlap** COMPORET E (216
25.54 identity in 216 as overlap** COMPORET E (216
25.54 identity in 216 as overlap** COMPORET E (211.2e-07)
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gene

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/db_xref="taxon:83332"
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78. .1481
                                                                                                                                                            Mycobacterium tuberculosis H37Rv.
Mycobacterium tuberculosis H37Rv
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1. .43401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="H37Rv"
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78. .164
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                                                                                              43401 hp
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                                                                                                            DEFINITION
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KEYWORDS
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PYVTANDIDARVLRRAGTRFANAPIRWLHADIMTAELPNAGFDAVVSNAALHHIEDTR
TALSRLGGLVTPGGTLAVVTFVTPSLRNGLWHLTSWVACGMANRVKGKWEHSAPIKWP
PPOTLHELREHVRALLPGACIRRLLYGRVLVTWRAPV"
                                                                                                          GREEYRAVKPGTPGIQPKGDMMYTVVDAGPGRVSRSYEVAAPAAEAELFAIVADPRRHR
ELDGSGTVRGNIKVPAKLVVGSKFSTKMKLFGLPYRITSRVTALKPNELVEWSHPLGH
RWRWDFESLSPTLTRVTETFDYHAAGAIKNGLKFYEMTGFAKSNAAGIEATLAKLSDQ
                                                                                                /translation="MSVYKHAPSRVRLRQTRSTVVKGRSGSLSWRRVRTGDLGLAVWG
                                                                                                                                                                                                                    /note="Rv0089, (MTCY251.07), len: 197. unknown, some similarity to spiP129991BLOC_ECOLI BIOTIN SYNTHESIS PROTEIN BLOC. (251 aa). FASTA scores: opt: 202 z-score: 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12406 GATCGGCCGAGGCGCACGTCAAAGTGATTCGCGCCTTTTTCGCCCACCTGCCCGCGCGG 12347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv0090, (MTCY251.08), len: 256. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                               6147. .6152
/note="abggag, potential rbs upstream of Rv0090"
6158. .6928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 38380;
        'note-"Rv0088, (MTCY251.06), len: 224. Unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/product="hypothetical protein Rv0090"
                                                                                                                                                                                                                                                                                                 /product-"hypothetical protein Rv0089"
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/db_xref="SWISS-PROT:010886"
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/protein_id=CAA98924.1"
/db_xref="G1:1405758"
/db_xref="SWISS-PROT:010885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.2%; Score 408.4; DB 1; 97.8%; Pred. No. 2.2e-56; ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv0090"
/gene="Rv0090"
6158. Ann
                                                                                                                                                                      5436. .6029
/gene="Rv0089"
5436. .6029
/gene="Rv0089"
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/gene="Rv0090"
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                         /codon_start=1
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Best Local S
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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markow Model of TB genes (mplemented in TBparse (kroyh) supplemented with visual inspection of positional base preference in codons, especially where there is an interess. In the observed/expected third position of 4C an interess. In the observed/expected third position of a correct initiation codon. Where possible we choose an initiation codon (algorithms) give sequence (optimally 5-13bp before the initiation codon pointing site sequence (optimally 5-13bp before the initiation codon codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculos is sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 15A Unite de Genetique Moleculaire Bacterienne, Institut pasteur, 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:2104370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole, S. T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S. V., Eiglmeler, K., Gas, S., Barry Ill, C.E.,
Harris, D., Gordon, S. V., Eiglmeler, K., Gas, S., Barry Ill, C.E.,
Tekais, F., Badcock, K., Basham, D., Chillingworth, T.,
Gontles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quall, M. A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Squares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B.G.
                    Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.
295390 AL123456
295390.1 G1:3261766
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Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deciphering the biology of Mycobacterium tuberculosis from the
03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv3448"
/note="PS00402 Binding-protein-dependent transport
systemsinner membrane comp signature"
                                                                                                                                                                                                                                                                                                                               Bacteria, Firmicutes; Actinobacteria; Actinobacteridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mycobacterium tuberculosis H37Rv"
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/strain="H37Rv"
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1 (bases 1 to 43401)
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Nature. 393 (6685), 537-544 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable precursor of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 053863 SERINEPROTEASE (199 aa) opt: 241; E(): 8e-07; (38.0% identity in387 aa overlap), similar to MTCX15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                      /db_xref="61:3261767"

Adb_xref="61:3261767"

/Lanslation="MapTsDpGLRWTWHAGAQAVDLTLPAAVPVATLIPSIVDILGDR
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GLAALLFAAVAACRTYRDPIAGLTLSVIATIFGAAVGGLLAVPGVPGVHSVLVAAMAAAAA
TSVLAMRITGGGGITLTAVACCAVVVAAATLVGAITAAPVAIGSLATLASFGLLEVS
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ROALAXAVDVKNAVIVAAAGNTGGAAQCPPQAFGVTRDSVYTAVSPAAVDDVLTVGS
VNAQGEPSAFTLAGPWVDVAATGEAVYTSLSPFGDGTVNRLGGOHGSIPLSGTSYAAPV
VSGLAALIRARFPTLTAROVMQRIESTAHHPPAGWDEVGNGTVDALAAVSSDSIPQA
GTATSDPAPVAVPVPRRSTPGPSDRRALHTAFAGAAICLLALMATLATASRRLRPGRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARMAVLLAGISPRLPPALNPDDADALPTTDRLTTRANRADAWITSLLAAFAASATIGA
IGTAVATHGIHRSSWGGIALAAVTGALLLERARSADTRRSLVFAIGGITTVATAFTVA
ADRALEHGPWIAALTAMLAAVAMFLGFVAPALSLSPVTYRTIELLECLALIAMVPLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MTTSRTURLLVVSALATLSGLGTPVAHAVSPPP HDERWLPESAL
PAPPRPTVQREVCTEVTAESGRAFGRAERSAQLADLDQVWRLTRGGGGRVAV1DTGVA
RHRRLPRVVAGGDYVFTGDGTADCDAHGTLVAGI1AAAPDAQSDNFSGVAPDVTL1S1
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                                                      Unknown membrane
                                            Jobe-"RV348, (MTCY77.20), len: 467 aa. Unknown membr
protein, contains PS00402 Binding-protein-dependent
transport systems inner membrane comp signature. Some
similarity to AL021930|MTV035_18 Mycobacterium
thebreculosis (472 aa) fasta score, opt: 429 z-score:
488.4 E(): 1.1e-19; 28.2%identity in 479 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="RV3449, (MTCY13E12.02), len: 455. Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mycobacterium tuberculosis H37Rv"
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/db_xref="GI:2104372"
/db_xref="SPTREMBL:006316"
                                                                                                                                                                                                                                                                                                   /product="hypothetical protein Rv3448"
/protein_id="CAB08736.1"
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1862. .1894
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/clone="Y13E12"
1478. .2845
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/transl_table=11
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/gene="Ry3449"
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/gene="Rv3449"
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VVVGPAEDSSAQVI/TAEQM ILVATESGSPTYLLYGGRRAVVDLADPAVVWALRLQGRV
PHVVAQSLLNAVPEARTITARRIRGGGRASVGLPGELVGGVNRITRASGDEYYVVLED
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RSAVVARRSLSGGGYGTRYLVTDTGVRFAIHDDDVAHDLGLPTAAIPAPWVLATLPS
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REVIAGESGGATVTO FVAGVPLGSTSFGSPLPAAYADNVAAVAVFGNPSNRAGGSLSS
TSFLEGSKATDLÜNFTOPTCHVGPGNPFSGHIDGYTPTYTYAAASFVVQRLRAGSVPH
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                                                                                                                                                                                                                                                                                                                                                                                                                ALGCYLATVAAMGCAFVALLRPQSALGQAPIVMGRESGALYVKVDDVWHPVLNLASAR
LLAATNANPQPVSESELGHTKRGPLLGIPGAPQLLDQPLAGAESAWAICDSDNGGSTT
                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MPSPATTWLHVSGYRFLLRRIECALLFGDVCAATGALRARTTSL
unknown but similar to Rv3895c MTCY15F10.17 (FASTA score: 16e-27; 36.4% identity in 475 as overlap); possible membrane spanning region near N-terminus, and to Y14967[MLCB628_16 Mycobacterium leprae cosmid B628; 481 as opt: 708 z score: 710.9 E(): 4.5e-32; 32.9% identity in 480 as overlap, also similar to Rv3869 (MYV0210.4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable cutinase, similar to several, contains cutinase, ser ine active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU Q50664 probable cutinase cy339.008c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCY13E12.05 (FASTA score: E(): 0; (59.2%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15625 GATCGGCGAGGCGCACGTCAAAGTGATTCGCGCCCTTTTTTCGCCCACCTGCCCGCGGG 15684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4049. .4081)
/qene="Rv3450c"
/not.e="PS00013 Prokaryotic membrane lipoprotein lipid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Rv3451, (MTCY13E12.04), len: 247. Function:
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/note-"possible RBS, GAGG, for Rv3452"
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                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:006317"
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5178. .5858
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97.8%;
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complement(3485. .4378)
/gene="MT3562"
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/yene-"MT3560"
/note-"identified
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                                                                                                                                                                              871. .1566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, D., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Rolony, J.F., DeBoy, R., Undayam, L.A., Ermolaeva, M., Hickey, E., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishal, W.

Submitted (25-ARP-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                               15685 TGGATGTGTCCACCCGCCAGGCCGGCGAAGCCGACCTGGCCGGCAAAGCCGCTCAATATC 15744
                                                                                                                     BCT 27-APR-2001
section 246 of 280 of the
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                                                             gtcccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacggcg
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Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

    16384
/organism-"Mycobacterium tuberculosis CDC1551"

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Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 16384)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            cacgacgggctgctggccgggctgcgcgctgatc 453
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Mycobacterium tuberculosis CDC1551,
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/codon_start=1
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AE007160 AE000516
AE007160.1 GI:13883389
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96. .839
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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G. JEGSYLL AGENT GEORGIA LEGITIVA DEPONDATE LEGITIVA DEPONDATION DE CONTROLL D /translation-"wiradimentary HFTGREVCGRANKFLGITSFAIALKKVDAGRHNKO" HFTGREVCGRANKFLGITSFAIALKKVDAGRHNKO" 185. :3523 1835. :3523 / rans_table=11
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I.SPLFGSKAIDICNPTDPICHVGPGNEFSGHIDDYIPTYTTQAASFVVQRLRAGSVPH /pub. 1738657: identitied by sequence similarity; putative" /codon_start-1 /hote-"similar to SP:000298; identified by sequence similarity; putative" //codon_start-1 /product="tRNA pseudouridine synthase A" /protein_id="AAK47901.1" /db_xref="GI:13883394" 1835. 3523 genee—"WHT3561" /note-"identified by Glimmer2; putative" /codon_start-1 by Glimmer2; putative" /product="hypothetical protein" /protein_id="AAK47899.1" /db_xref-"G1:13883392" 1.PGSVPQLPGSVLQMPGTAAPAPESLHGR

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CDS

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TRYNRRTRGKFGFRTIACKKRAR"
COMplement (7719)
/gene="MT3567.1"
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                                                                     complement(7719. .7832)

Agene-MT3567.1"
//note--8.imilar to SP:P45810; identified by sequence similarity; putalive"
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Pred. No. 1.8e-55;
); Mismatches 9;
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Pred. No. 1.3e-49;
0; Mismatches 12
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Stover, C. Kendall and Mahairas, G.G.
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ilarity 97.18;
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complement(7129. .7503)
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similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase,
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complement(4897. .5940)
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complement(6092..6697)
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 aggcgcacatcaaagtgattcgcgccctttttcgccc--acctgcccgccgcgtggatg
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Pred. No. 1.4e-46;
0; Mismatches 5;
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US 6008201
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258 c 185 a
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Sequence 5 from patent 1
AR096715
AR096715.1 GI:10025753
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Local Similarity 97.7%;
tes 388; Conservative
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Riley, L.W.
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Riley, L.W. and Choug, P.
DNA molecule tragments encoding for cellular
mycobacterium tuberculosis and uses thereof
Patent: US 6224881-A 5 01-MAY-2001;
                                                                                                                                                                       PAT
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llarity 97.7%; Pred. No. 1.4e-46;
Conservative 0; Mismatches 5;
                                                                                                    ccacgacgggctgctggccgggctgcgcgcgctgatc 453
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Sequence 5 from patent US 6224881.
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/organism-"unknown"
258 c 185 q
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2, 2002, 22:45:52

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AE007028 Mycobacte
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: April 2, 2002, 19:17:10 ; Search time 2977.34 Seconds (without alignments) 7718.491 Million cell updates/sec	Title: US-09-785-904-1 Perfect score: 1393 Sequence: 1 tgggttcgggtagccgcgaacgacgacaaacccgattgac 1393	Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0	Searched: 1472140 segs, 8248589755 residues	umber of hits sa	Minimum DB sec lergth: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:*			9. 95_pr.: 9. 9b_pr.:* 10. ab_ro:*		13: 92-01: 13: 95-un:* 14: 95-un:*		20: em_Ou:* 21: em_ov:* 22: em_pat:*	23: em_ph:* 24: em_pl:* 25: em_pt:*					

U00021 Mycobacter 256891 Mycobacter 256801 Mycobacter Continuation (4 of AC090554 Mys muscu AL58991 Mycobacte AL021428 Mycobacte AL022022 Mycobacte AC021428 Mycobacte AC081799 Mus muscu AL17857 Homo sapi AC046159 Homo sapi AC04159 Homo sapi AC04159 Homo sapi AC031928 Xylella f

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mycobacterium tuberculosis H37Rv.

Mycobacterium tuberculosis H37Rv

Mycobacterium tuberculosis H37Rv

Actinomycetales; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriums; Mycobacterium tuberculosis complex.

Bycobacterium: Mycobacterium tuberculosis complex.

Color, S.T., Hossch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Biglmeder, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davlies, K., Teltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A., Rajandream, M. A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., or 03-AUG-2001 genome; segment 147/162. complete H37Rv MTY13E12 43401 bp DNA Mycobacterium tuberculosis F 295390 AL123456 295390.1 G1:3261766 SULT 1 Y13E12 CUS CUS FINITION CESSION RSION RGANISM FRENCE

ALIGNMENTS

MTV023 AC084799 AL137857 AC046159 AC034105

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GLAALLPAVIACRTYRDPIAGLTLSVIATIFGAVAGLLAVPGVPEVHSVLVAAMAAAA
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ARMAVLLAGLSPRLPPALNPDDADALPTTDRLTTRARRADANITSLLAAFAASATIGA
IGTAVATHGIHRSSMGGIALAAVTGALLLRARSADTRRSLVFAICGITTVATAFTVA
ADRALEHGWNIAALTAAMLAAVAMFLGFVAPALSLSPVTYRTIELLECLALIANVPLTA
WLCGAYSAVRHLDLTWT"
                                                                                                                                                                                                                                             Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2104370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CANTION: In some cases we may not have predicted the correct
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Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
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                                                                   Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rv3448, (MTCY77.20), len: 467 aa. Unknown me
protein, contains PS00402 Binding-protein-dependent
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/ystemsinner membrane comp signature"
78. .1481
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/organism="Mycobacterium tuberculosis H37Rv"
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                                                                                                     complete genome sequence
Nature. 393 (6685), 537-544 (1998)
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78. .164
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probable precursor of serine protease. Has putative signal peptideat N-terminus and hydrophobic stretch at C-terminus. Contains three signatures typical of subtilase family: aspartic acid active site (PS00136), histidine active site (PS00137), serine active site (PS00138). FASTA results: 9G3863 sERINEPROTASE (390 aa) port: 241; E(): 8e-07; (38.0% identity in 87 aa overlap), similar to MTCY15F10.29 (45.7% identity in 451 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSSSKEAPVGDPSSTGVGDVDTMARAVRTAADLGASVINISSIACVPAAAAPDDRAL
GAALAYAVDKNAVIVAAGNTGGAAQCPPQAFGVTRDSVTVAAVSPAWYDLYUTGGA
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CTATSDPAPVAVPPRRSTPGPSDRRALHTAFAGAAICLLALMATLATASRRLKPGRN
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GRAVTTLCVTWTPAOPGAARVAFLAGSGPPVPLGGVPVTLAQADGRGPALDAVYLPPG
RSAYVAARSLSGGGTGTRYLVTDTGVRFAIHDDDVAHDLGLPTAAIPAPWPVLATLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note."PS00138 Serine proteases, subtilase family, serine active site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4049, .4081)
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/note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                 (MTCY13E12.02), len: 455. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"PS00137 Serine proteases, subtilase family, histidine active site" 2456 - 2488 /qcne-"kv3449"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="PS00136 Serine proteases, subtilase family,
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MTU43540 3453 bp DNA BCT 14-AUG-1997 Mycobacterium tuberculosis rfbA, rhamnose biosynthesis protein (rfbA), and rmlC genes, complete cds. U43540 U43540 GI:2326948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                       probable cutinase, similar to several, contains cutinase, serime active site motif (PS00155). Alternative start possible at 3733. FASTA results: CUT2_MYCTU Q50664 probable cutinase cy339.08c precursor (219 aa) opt: 565; E(): 2.3e-26; (44.8% identity in 223 aa overlap). Also similar to MTCU3E12.05 (FASTA score: E(): 0; (59.2% identity in 211 aa overlap).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctogtogagoactcacoggtgaacogctagecccacagttgacogcacogccacogcc 360
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probable cutinase precursor. Contains PS00155 Cutinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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; Pred. No. 5.4e-181;
0; Mismatches 0;
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5178...5888
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4388. 5131
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2202. .2655
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee,T.
Direct Submission
Submitted (18-DEC-1995) Tae-Yoon Lee, Microbiology, College of
Medicine, Yeungnam University, 317-1, Daemyungdong, Namku, Taegu
7 (5-035, South Korea
3 (bases 1 to 3453)
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Namku, Taegu
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                                                                                                                                                                                                                                                                   Rhamnose biosynthetic genes related to a novel repeated Mycobacterium tuberculosis
                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaee; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology,
Daemyungdong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee, T.

Direct Submission

Burnect Submission

Submitted (14-Aug-1997) Tae-Yoon Lee, Microbiology,

Medicine, Yeungnam University, 317-1, Daemyungdong,
705-035, South Korea

Sequence update by submitter
On Aug 14, 1997 this sequence version replaced gi::

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Mycobacterium tuberculosis. Mycobacterium tuberculosis
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           3; Gaps
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Score 1354.2; DB 1; Length 3453; Pred. No. 3.2e-175; 0; Mismatches 8; Indels 3;
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Best Local Similarity 99.2%;
Matches 1382; Conservative 0
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/note="3-4 copies in M. tuberculosis genome: Found in the rfb cluster (inside the rfbA gene), also found in the mce of M. tuberculosis; present at 3-4 sites of the genome of H37Rv, H37Ra, Erdman, and many isolates; not found in M. smeqmatis & M. avium."

06. .2250 990 g

/rpt_type=dispersed /rpt_unit=1806, .229 | 1226 c 990 g

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BASE CO ORIGIN

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2668 CTGGGCCAACACAACGTCTTCCCGTCTCGATGGTGACCACCACCAGCTGACCTG	<pre>UY 901 caaaccggccaggcaagggcttcaccggcggcggcacctgctacccatggccgatgtg 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</pre>		2788 ATCCGCATGACCAGCCCACCACCACTACTCCCCCGCAAGCGGGAGGTACCCCCAGGCG	VY 1041 atoticgaccacggcacaccctggcgctgtatcacaccaaacgcctagcctccccggcc 1080	QY 1081 cagcggatcatgctgttcgccaacgaccgccggctgcaacccgcctgtgacgcaccg 1140 Db 2908 CAGCGGATCATGCTTCGCCAACGACCGCGCTCCAAACCCGGCTTGACGCACG 2967		1201	3028	Qy 1261 cacaaccacaggccaccgcactgctaccacccaccccac	QY 1321 cccgcaccaacacttccaccagaacgattcttccacaaccaagacgacgacgac 1380	1393		RESULT 3		complete genome. AE007028 AE000516	NDS	SOURCE Mycobacterium tuberculosis CDC1551. ORGANISM Mycobacterium tuberculosis CDC1551	Bacteria; Firmicutes; Actinobacteria; Actinobacteridee; Actinomycetales; Corpubacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberiunsis complex	REFERENCE 1 (bases 1 to 17783) AUTHORS Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.	Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolomay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salyhero, S. J., Dalcher A. Itterheim, W. C., Maisham, R. Marian, M. C., Maisham, M. C., Maish	Glll,J., Mikula,A. and Bishai,W. TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and	JOURNAL Upoublished	to 17783) R.D., Alada, D., Eisen, J.A., Carpenter, L., Whi	KolomayJ.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Hiterback,T., Weinman, I., Whomer, U.	Gill,J., Mikula,A. and Bishai,W. Direct Submission	JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA	rce

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SRRPL"
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KTVLI PDORAGCSLADS TPDELRAWKDEHPGAVVVSYVNTTAAVKALTDICCTSSNA
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                                                                                 Submitted (07-JAN-1998) Microbiology & Immunology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10010, USA Location/Oualifiers
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1 (bases 1 to 10019)

Yu, S. and Jacobs, W.R. Jr.
Cloning, sequencing, and identification of Mycobacterium bovis BCG biotin biosynthetic genes by complementing two Mycobacterium
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Pred. No. 3.1e-170;
0; Mismatches 42;
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/transl_table=11
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Best Local Similarity 97.0%;
Matches 1341; Conservative
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YPQAIPDHGTPLALYHTKRLASPAQRIMLFANDRGCTKPGCDAPAYHSQAHHYTGWTS
TGRTDITDLACDPURLAEKGWTTRKNTHGHTEWLPPPHLDHGQPRTNTFHHHEKL
LRHNDEDNHDDP"
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/gene="bioB"
7455. .8504
/gene="bioB; similar to MTCX336.15c"
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Mycobacterium tuberculosis CDC1551

Mycobacterium tuberculosis CDC1551

Bacteria; Firmicutes; Actinobacteria; Actinobacteriaceae;
Actinomycetales: Corynebacterineae; Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Mycobacterium: Unberculosis complex.

E 1 (bases 1 to 16384)

S Fleischmann, R.D., Alland, D., Bisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Oson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.

Haboratory strains
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                                                                                                                                                          6220 CGCAACCACGACGGGCTGCTGGCCGGGCTGCGCGCGCTGATCGCCTCCGGGGAACTGGGC
                                                                                                                    6160 CAACACAACGTCTTCCCGTCTCGATCGTGTCACCACCACCACCACCACCACCTGAAACC
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                                                                                                    Mycobacterium tuberculosis CDC1551,
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AE007160 AE000516
AE007160.1 GI:13883389
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DDHIAAAALFGNPSGRAGGLMSALTPQFGSKTINLCNNGDPICSDGNRWRAHLGYVPG
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Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9711
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
1. 16384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to SP:Q00298; identified by sequence similarity; putative" /codon_start=1
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us-09-785-904-1.rge

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Complement(131562"

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/ Gote="MT3562"

/ Gote="MT3562"

/ Gote="MT3562"

/ Codon_start=1

/ transl_table=11

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/ translation="MSITRAPPERPRESSOVALENDIAYDEAGNAQUO

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RTVAGDLDAATTERTPAPERSPORPERISGOVAHUDYPABALDHAPPRAGUG

RYTAMPREDLDAWTAASRDLMGLHAPFARFERSTRINGCALDARGEALRENGTINDLMSRAGTLNTA

HVTADAFCWSWYRSLVGALAYGEHRRATTWCRELLTATGRSSDFAVAPAHGLTLIGV

COMPLement(4323. .4865)

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PID:42800; identified by sequence similarity; putative"

/ control and a product of the sequence similarity; putative"
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GGLGAALQPYSPLVAIVTALVMPPILAAATKGKYYLRRTHDGIDLPMYDEHGNBSAAV
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COMPLement (3485. 4378)
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Complement (3485. 4378)
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complement(#897.5940)
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STRANGVLHEFTYPOFGWEDVTEILLNLKSLYWSSEDEEPVTMYLRKOGP
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ARTESDLINDRAKGIETGPSPARADHIASFALLDIDLIHTYNRSYNCILKREGVRIPYGELL
AYDEQDYABTEGOL
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EYLLOLOEKOKARFTYGVMEKOFRRYYEEAVROPGKTGEELLKILESRLDNYIYRAGL
ARTRRMAROLUSHGHFNVNGVHVNVPSYRVSQYDIVDVRDKSLNTVPFQIARETAGER
PIPSWLOVYGERORVLIHOLPERAQIDVPLTEQLIVEYYSK"
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/notedous.attel
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complement(6092..6697)
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CDS

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Complement(7129. .7503)

Agene="Mr3567"

Anote="similar to GP:21043%; identified by sequence similarity; putative"

Codon_start=1

Arodor="ribosomal protein S13"

Aproduct="ribosomal protein S13"

Ab_xref="id" AAK47996.1"

Ab_xref="id" AAK47996.1"

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TTPPQGAGLEVGAISIVTPQPHNGVRPPKRRV"
complement(7129. .7503)
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                                                                                                                                                                                                                                                                                              /note="similar to SP:P45810; identified by similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                   Score 1315; DB 1;
Pred. No. 3.2e-170;
0; Mismatches 20;
                                  $11"
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similarity; putative"
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Best Local Similarity 98.5%;
Matches 1327; Conservative
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Direct Submission
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and
                                                     Hickey, Molecular
Ave. W., Seattle,
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Singh, D.C.
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No. 1.2e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
                                                                                                                                                                       bovis
  Hickey, M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1314.2;
Pred. No. 1.2e
0; Mismatches
                                                                                                                                                        /organism-"Mycobacterium
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1400
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; 0

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.3019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="H37kv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv1565c"
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/note="Rv1565c"
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complement(2327.
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/transl_table-11
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AUTHORS
TITLE
JOURNAL
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Mycobacterium; Mycobacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

( bases 1 to 32437)

( cole,S.T. Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
Hamlin,N., Holroyd,S., Devlin,K., Feltwell,T., Gentles,S.,
Houne,S., Murphy,L., Oliver,S., Osborne,J., Quali,M.A.,
Rajandream,M.A., Rogers,J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Squares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYCODACTERIUM tuberculosis H37Rv complete genome; sequent 70/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctgaccctggcctgcggccccgacaaccgactcgccgaaaaaggctggaccaccacaaac 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1284 CTCACCCTGGCCTGCGACCCCGACAACGACTGGAAAAAGGCTGGACCACCGCAAA 1343
                                                                                                                                                                                                                                                                        1086
                                                                                                                                            gegeceggcaaggettcaccggeggegcacctgctacccatggccgatgtgatccgc 966
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                                                                                                                                                                                                                                                                                                      1163
                                                                                               gaccacggcacacccctggcgctgtatcacaccaaacgcctagcctccccggcccagcgg
                                    cgcaaccacgacgggctgctggccgggctgcgcgcgctgatcgcctccgggaaactgggc
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature. 393 (6685), 537-544 (1998)
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Z95586.1 GI:3261785
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LOCUS
DEFINITION
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VERSION
KEYWORDS
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/tians_Leau_id="""
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Parkhill,J.

Direct Submission

Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CBIO 1SA Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
No Jun 27, 1998 this sequence version replaced gi:2117233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have ulter renumbered from the original cosmid submissions but the old gene designations are in brackets after the may gene numbers.

Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon where possible we choose an initiation codon where possible we choose an initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism~"Myrobacterium tuberculosis H37Rv"
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/organism-"Mywobacterium tuberculosis H37Rv"
/strain-"H37Rv"
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393 aa overlap
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6258. .6938
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/gene-"biof"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.9%;
98.4%;
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Best Local Similarity 98.4
Matches 1320; Conservative
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TFLAMSICDPHGGMHSLWTDVLAAQVFAPQVPRDYDPAYSAAFEAQLAQHAGELAAVV
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PYLVRWLGTOPTPVQQAPKGDLIFYGPEGTGSYALYLGKGQMLEVGDVVQVSPVRTNGMT
VQPPPFGTARSR"
                    probably exported has QOAPV repeats at C-terminus, similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Jote="R27568, (MTCY336.35c), bioA, len: 437. Function: probable adenosylmethionine-8-amino-7-oxonomanoate aminotransferase (EC2.6.1.62) 006622. Contrains aminotransferase class-III pyridoxal-phosphate attachment site (PS00600). FASTAresults, BIOA_MYCLE P4548 (436 aa) sixie (PS00600). FASTAresults, BIOA_MYCLE P4548 (436 aa) similar to other M. tuberculosis proteins e.g. denity in 421 aa overlap. TBparse scoreis0.874"
                                           to hypothetical M. leprae protein, to putative invasins 1,2(007390, 007391) from M. avium and slightly similar to C-terminus of Listeria invasion-associated protein p60 precursor P60_Lister p60 precursor P60_Lister P60_E180 p1170 (246aa) opt: 957 E(): 0; 70.0% identity in 207 aa overlap. TBparse scoreis 0.890"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv1567c, (MTCY336.36), len: 94. Unknown. TBparse
score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="possible RBS, AAGGAGG, for Rv1566c"
comptement(3258. .3263)
//note="ASNI site: ATTAAT; probably linking fragments
B3/G6"
/note-"Rv1566c, (MTCY336.37), len: 230. Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00600 Aminotransferases class-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyridoxal-phosphate attachment site" 5101. 6261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3259. .3543)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(3259. .3543)
/gene="Rv1567c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3030.
                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv1567c"
                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3791. .5104
/gene="bioA"
3791. .5104
/gene="bioA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4541. .4654
/gene="bioA"
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5101. .6261
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/ LTAIGS LATION="MKAATQARIDDSPLAMLDAVQRORHEAGLRRCLRPRPAVATELD
LASNDYLGLSRHPAVIDGGVQALRIWGAGATGSRLVTGDTKLHQOFE&RLAEFVGAAA
GLLFSGGYTANIGAWVGLSGPGSLLVSDARSHRSLVDACRLSRARVVYTPHRDVDAVD
AALRSRDEGRAVVYTDSVRSADGSLAPVRELLEVCRRHGALLLVDEARIGGVRGGGRG
LLYELGIAGAPDVVATTLSRALGSGGGVVLGPTPVRAHLIDAARPFIFDTGLAPAAV
GAARAALRVLQAEPWRPQAVLNHAGELARMCGVAAVDDSAMYSVILGFPESAYAAAAA
CLIDAGVKVGCFRPPTVPAGTSRLTTARASLNAGELELARRVLTDVLAVRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
/note="Rv1569, (MTCY336.34c), bioF, len: 386. Function: probable 8-amino-7-oxononanoate synthase (EC 2.3.1.47) 006621. Contains aminotransferases class-II pyridoxal-phosphate attachment site (PS00599). FASTA results, BIOF_MYCLE P4548/1385 aa) opt: 1971; E(): 0; 80.18 identity in 381 aa overlap. Also similar to MTCY10H4.32, FASTA score: E(): 5.5e-29;37.4% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gacggcgactcaccgacaccgaacgcgcacagcaaacgcggcatcaccctgagcaaccag 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgggtagccgcgaacggattgtcgaggtctttgatgcgctggatgccgagctggaccgct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cccaagerageqqqqaqqaartqqqqqqqqcqctqcqqcqqqtqac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 32437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                   /note-"PS00599 Aminotransferases class-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5e-169;
                                                                                                                                                                                         /protein_id="CAB09068.1"
/db_xref="G1:2117258"
/db_xref="SW1SS-PROT:006621"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1307.4;
Pred. No. 2.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                        /codon_start=1
/transl_table=11
/product="biof"
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Wed Apr

us-09-785-904-1.rge

	Notes: Details of M. Luberculosis sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base predictence in codons, especially where there is an increase in the observed/expected third position G to CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (arg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream initial or	Trocation/Qualifiers 1. 38380 /organism="Mycobacterium tuberculosis H37kv" /strain="H37kv" /strain="H37kv" /strain="H37kv" /db_xref="taxon:8332" /db_xref="taxon:83312" /db_xref="taxon:83312" /clone="taxon:83312"	/qcne="hycu" /qcne="hycu" /qcne="hycu" /qcne="ky0084, (MTCY251.02), len: 316,hycD, similar to HYCD_EXCOLD PLAG LOTMate hydrogenlyase subunit 4 (307 aa) FASTA SCOLES, upt: 570, score: 591.6, E(): 2.1e-26, (4.4.8% identity in 405 ac overlap) and NUOILECOLT F1460 hadowerlap) cold acoverlap) /ccdon_start=1 /transl_table=11 /ccdon_start=1 /transl_table=11 /product="hycD" /db_xref="G1:1405754" /db_xref="G1:1405754"	DLLKOLGKQOITPAGTTIVPAAPVIVAGTTLLIAAAAPLWATGSPLDPSADLEAVUR ELECTVALTLAGIDTGTSFGGGGASRETTLALABATPLWATGSPLDPSADLEAVUR LEFGTVALTLAGIDTGTSFGGGGASRETTAALWEPTILLAVFALSIPAGSANLGAL VASTIDHPGHVVSLAGVLAFVALVIVLAGATGRAPTHLELTWHEAMVLEYAG PRIALVEWAAGMRLVVLALLANIELPWGIAGAAPTALLDVITGVVAVAAKVAILAVLL ATFEVFLAKIRLFRVPELLAGSFLIALAVTAANFFTVGA" 967. 1629 967. 1629 967. 1629 9680e="hycp" 700te="Rv0085, (MTCY251.03), len: 220. hycp, similar to SpIP77524 HYFE,ECOLI HYDROGENASE-4 COMPONENT E (216 aa),FASTA scores: opt: 204 z-score: 272.1 E():1.2e-07; 25.5% identity in 216 aa overlap"
TITLE JOURNAL MEDLINE REFRENCE AUTHORS TITLE JOURNAL		FEATURES SOURCE SOURCE GOORGE GENERAL CORS		gene
Qy 607 caatacgacggcatgtcacggctaagtggctacctgacccccaagggggccaccttt 666 Db 17628 CAATACGACGACTGTCACGCTAAGTGCTGACCCCCCAAGCGCGGCCACTTT 17569 Qy 667 gaagccgtgctagccaaactggccgccccgggcgaccaaccccgacgaccacccccg 726 Illillillillillillillillillillillillilli	Qy 847 caacacaaggtcttccgtctcgatcgtggtcaccaccctgaccgacc		SUL SUL CY2 COS COS STIN	Norder Mycobacterium tuberculosis H37Rv. ORGANISM Mycobacterium tuberculosis H37Rv. Bacteria; Firmicutes; Actinobacteria; Actinobacteriadae; Actinomycetales; Corynebacterium tuberculosis complex. Mycobacterium; Mycobacterium tuberculosis complex. Mycobacterium; Mycobacterium tuberculosis complex. Mycobacterium; Mycobacterium tuberculosis complex. Mycobacterium; Mycobacterium tuberculosis complex. Tobacterium; Mycobacterium tuberculosis complex. Mycobacterium; Mycobacterium tuberculosis complex. Tobacterium; Mycobacterium tuberculosis complex. Tobacterium; Marchill, J., Garnier, T., Churcher, C., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feitwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,

gene

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gene

gene

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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/product="hypothetical protein Rv0089"
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/db_xref="cir:1405759"
/db_xref="ion:1405759"
/db_xref="ion:1405759
                                                                                                                              /translation-"MSVYKHAPSRVRLRQTRSTVVKGRSGSLSWRRVRTGDLGLAVWG
                                                                                                                                                                                                                                                                                                                                                                                                       /note--Rv0089, (MTCY251.07), len: 197 unknown, some similarity to sp[P12999]BIOC_ECOLT BIOTIN SYNTHESIS PROTEIN BIOC. (251 aa). FASTA scores: opt: 202 z-score: 262.0 E(): 4.5e-07; 39.0% identity in 118 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 tegaatecttuuleegeggetervaksydteggteacgegttgatcaaccaacttgacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6147. .6152
/note="aaggag, potential rbs upstream of Rv0090"
6158. .6928
/gene="Rv0090"
6158. .6928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note*"Rv0090, (MTCY251.08), len: 256. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1301.4; DB 1; Length 38380;
Pred. No. 1.5e-168;
0; Mismatches 46; Indels 1;
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5436. .6n?
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/gene="Rv0090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 96.6%;
Conservative
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Matches 1340;
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lson, B., Garpenter, L., White, O., Ison, R., Gwinn, M., Haft, D., Hickey, E., Unayam, L.A., Ermolaeva, M., Utterback, T., Weidman, J., Khouri, H., Hai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRIIAPSKVKLKUTRSTVVKGKSGSI,SWKKVRTGDLGLAVWG
SOMMTVYVVOKAGENGSKSSVEVKADAAELEN I VADPRKHK
VVGSKESTKMKLEGLPY I TSRVTALKPUELSHPLGII
STEDYHAAGA I KNGLKFYEMTGFAKSNAAJ I EATI AKKLSDO
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TRANAPIRHHADIMTAELPNAGFDAVSNAALHHIEDTR
VTPVTPSLRNGLMHTSWVACGMANRVKCKWEHSAPIKWP
ACIRRLLYGRVLVTWRAPV*
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                                                                                                                                                                                                                                                                                                                                                                    Eisen, J.A., Carpenter, L., White, O., Son, R., Gwinn, M., Haft, D., Hickey, E., Umayam, L.A., Ermolaeva, M., Utterback, T., Weidman, J., Khouri, H.,
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le, MD 20850, USA
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terineae, Mycobacteriaceae,
um tuberculosis complex.
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is not the result of a sequencing artifact; identified by
Glimmer; putative; conserved hypothetical protein,
authentic frameshift"
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; Mismatches 48;
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Best Local Similarity 96.5%;
Matches 1338; Conservative C
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sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                            3791. .4162
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3791. .4162
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complement(7337. .8185)
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 9281)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh,D.C. and Molecular analysis of genetic differences between Mycobovis BCG and Virulent M. bovis
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, Seattle,
                                                                                  Singh, D.C.
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2 (bases 1 to 9281)
Mahairas,G.G., Sabo,P.J., Hickey,M.J., Singh, Direct Submission
Submitted (29-AUG-1995) Mark J. Hickey, Mole PathoGenesis Corp., 201 Elliott Ave. W., Sea 1. 9281
Location/Qualitiers
I. 9281
//organism-"Mycobacterium bovis"
//db_xref="taxon:1765"
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//note-"absent in related avirulent
//note-"absent in related avirulent
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Best Local Similarity 97.2%;
Matches 1304; Conservative
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DNA deletion

Mycobacterium bovis de, U35017.1 GI:10A027

DEFINITION ACCESSION VERSION KEYWORDS SEGMENT

MBDR3S1

of 2

SOURCE ORGANISM

Mycobacterium bovis. Mycobacterium bovis Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Db 744 GAAGCCGTGCTAGCC	0	oy	7
727 gtcatcgacaccacc	en v	<u>a</u> à	3AATAGCCGGGGGGGGGGTTGTCGAGGTCTTTGATGCGCTGGATGCCCGGGCTGGCT
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186264 Sequence 1	12412 bp DNA PAT 10-JUN-1998 From patent US 5700683.	Qy Db	720 caccedulical characterenegal grupocaceateracegegacacenyeageca 779 HHTHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
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SOURCE Unknown. ORGANISM Unknown. Unclassified REFERENCE 1 (bases 1	Unknown. Unknown. Unclassified. 1 (bases 1 to 12412)	OY OB	
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	86.3%; Score 1202.4; DB 6; Length 12412;	Qy	1020 gatettegaecaeggeaeaecectggegetgtateaeaecaaaegeetageteeeegge 1079
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(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes: Mactionbacteria; Actinobacteridae;
Bacteria; Firmicutes: Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Actinomycetales; Corynebacterium tuberculosis complex.
Mycobacterium; Mycobacterium tuberculosis complex.

E 1 (bases 1 to-3431)
Cole,S.T. Brosch,R., Parkhill,J., Garnier,T., Churcher,C.,
Harris,D., Gordon,S.V., Eiglmeier,K., Gas,S., Barry III,C.E.,
Tekaia,F., Badcock,K., Basham,D., Brown,D., Chillingworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Moules,S., Murphy,L., Oliver,S., Coborne,J., Quail,M.A.,
Royers,J., Rutter,S., Seeger,K., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence
L. Nature. 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted on behalf of the Mycobacterium Submitted (11-JUW-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur. 28 rue du Docteur Roux, 75724 paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced 9::217171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis H37Rv complete genome; segment 50/162. 295584 AL123456 295584.1 GI:3261774
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/db_xref="SPTREMBL:006536"
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DKSLCAGADLKAIARRENPYHPHHGEWGIAGYRHHFIDKPTSAAVSGTALDDGAEPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="cab09023.1"
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/db_xref="SPTREMBL:006535"
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YAYDPILLYANANHIQLYSIJULSNILFGONAPAIAAATEAAYEQUAADVAAMAVYSHISGASA
VAAQLAPWAQANHIPIPIPIPAASGPAALAIPAALPAATGIGNIGINIFSIGNIGDYNIGIN
ONIGNANIJOSIJATGAANIASGRAATAAPAATGIGNIGNIJALGSGNIGONIG
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NLAJ ANLONIN I GLUFGUNMIG LÖALANS JENLÖFONSGUNN I GLENSGNIN I GFEN
SCHSINFGFENSGUT INTGEGNAGETINFGFGNAGSGNFGFGNAGNINFGFGNSGFENMGV
GNSØAYNTGSFINSCTLINTGDLINSGDFNTGMANSGDINFGGFFISGDLINFGFGSEVVDQPV
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NTGLFNTGFNNTG1GNSATNAAFTTTSGVANSGDNSSGGFNAGNDQSGFFING"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaAsn, rich family (PPE class). Similar to etc,
MTCY98.0034c,MTCY0377.23, MTCY13E10.17c, MTCY06H11.05,
MTCY98.006c. FASTAGACORES: MTCY9824 NID: 91781238 -
MYCODDACTETIUM LUDERCULOSIS (615 aa) opt: 2292: E(): 0;
59.6% identity in 627 aa overlap. TBparse score is 0.881"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2805. .3146
/gene="Rv1136"
2805. .3146
/gene="Rv1136"
/note="Rv1136, (MTC165.03), len: 113. Some similarity to
N-terminus of carnitine racemases and ENOYL-COA
HYDRATASES.FASTA scores: 141014 carnitine racemase -
Escherichia coil(297 aa) opt: 258; E(): 2.58-11; 44.5%
identity in 110 aaoverlap. TBparse score is 0.871"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Rv1135c, (MTCI65.02c), len: 618. Member of Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Rv1134, (MTC165.01), len: 78. TBparse score is
                                                                                                                                                                                                                                     /organism-"Mycobacterium tuberculosis H37Rv"
                                                                 /organism~"Mycobacterium tuberculosis H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="possible RBS, AAGG, for Rv1135c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPYEAADLDEQGPFPMETVYLWEDGPNGTTRMTL"
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                                                                                                                                                                                                                                                                                                           /db_xref="taxon:83332"
/clone="165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(471. .2327)
/gene="PPE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(471. .2327)
/gene="PPE"
/db_xref="taxon:83332"
                                                                                                                               /db_xref="taxon:83332"
/clone="Y22G8"
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Gaps

25;

15743

120

15683

300

180

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15383 GCCACCAGTUGGGGTCCCGATGACTGGCTGGCTGGCCACGCAGCTGATGGACTGGCTG 15324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15802 CGCGGGTGCTCGATCTCAAGTGCGTTGACCACCCCGGAATTGCTGGCCTGTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 accgettygacyaygtgtettttgagqtgttgaceaececeagaacggetgcggtetetgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggttacgcatcarraagcccgacgccgccggcgcgcatcgccgacgccgatctcqqac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttgacycccaaqcraycgaggaaqaartgggcargctgtgctgcgcgctggccaacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721 accceggicalequeacecececegalqegecegecalegaecegegaeacecegeagecaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14963 GAAGCCGCCACCGCCAAGGGGTAACCGGTGGTTCGCGGGTGCCGATGTCGGACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 ctgcccqccqcqqqtqqatgtgtccaccqccaggccqccgaagccgacctggccggcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            781 geccaacycaaccacgacgggctgctgqccgggctgcgcgcgctgatcgcctccgggaaa
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                                                                                                                                                                                                   Length 34331
                                                                                                                                                                                                                                                                         384; Indels
                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                    699.6; DB
                                                                                                                                                                                                                                                                                        0; Mismatches
/protein_id="CAB09028.1"
/db_xref="G1:2117178"
/db_xref="SPTREMBL:006540"
                                                                                                                                                                                                   Score
Pred.
                                                                                                                                                                                                   50.2%;
                                                                                                                                                                                                                                           70.48;
                                                                                                                                                                                                                                                                                             Conservative
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HHLQDASRGHARGCGPLRQVVSRRYAGRVLLVGDAAGYEDALTGEGISLAVKQAAAAV
SAIVDDTPASYEAAWHRITRDYRLVTRGLVLASTPRAARRAIVPLCALLPTAFRYGVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLSARCHIRHIGSPGKDARCAHLSATLRPGIGISPTNVGNATVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"hypothetical protein Rv1139c"
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/db_xref-"SPTERBH:06539"
/translation-"MYYLLILAVVFERLAELVVAQRNARWSFAQGGKEFGRPHYVVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5546. 6394
/gene="Rv1140"
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/cote="Rv1140"
/cote="Rv1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILHTALLLGCVVEPWALHRPFIPWLGWPMLAVVVÄSOGLRWWCYKSLGKRWNTRVIVL
PHATLVRRGPYRWMRHPNYVAVVAEGFALPLVHTAWLTALVFTLANATLLTVRLRVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4684. .5184)
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complement(4684. .5184)
/gene="Rv1139c"
/note="Rv1139c"
/note="Rv1139c
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M.tuberculosis hypothetical proteins e.g. TR:P72008
MTCV4C12.35 (412 aa), fasta scores; opt: 89 z-score:
292.1 E(): 4.5e-09, 24.6% identity in 358 aa overlap.
TBparse score is 0.929"
                                                                                                                                                                                                                            /note="Rv1137c, (MTC165.04c), len: 122. unknown"
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5546. 6394
                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein Rv1137c"
/protein_id="CaB09025.1"
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/transl_table=11
/product="hypothetical protein Rv1140"
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/note="possible RBS, AGGA, fc
complement(3671..4687)
/gene="Rv1138c"
/gene="Rv1138c"
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                                                                                                                                  complement(3286. .3654)
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/transl_table=11
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                                                                                                                                                                               /gene="Rv1137c"
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(pases 1 to 14953)
Fleischmann,R.D., Alland,D., Eisen,J.A., Carpcutter,L., White,O.,
Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Hatt,b., Hickey,E.,
Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M.,
Salzbergy,S.L., Delcher,A., Utterback,T., Weidman,J., Kheuri,H.,
Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
   | |||
|-----TCTGGCA 14868
                                                                                                                                               14867 TIGITIGACGCCCTAAGCCGTIGCGTIGTATCACACCAAGCGGTIAGCTICCCCGGCC 14808
                                                                                                                                                                                                                       Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers
                                                      atcttcgaccacggcacacccctggcgctgtatcacaccaaacgcctagcctccccggcc 1080
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                                                                                                                                                                                                                                                                               accgayctgaccctggcctgcygccccgacaaccgactcgccgaaaaaaggctggaccacc 1260
                                                                                                                                                                                                                                                                                                                                                     cacaacaacacccacggccacaccgaatggctaccaccaccccacctcgaccacggccaa 1320
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Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O., Fleischmann,R.D., Alland,D., Eisen,J.A., Faft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayan,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Direct Submission
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                                                                                                                              cagoggatcatgctgttcgccaacgaccgcggctgcaccaaacccggctgtgacgcaccg
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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complement(172. .390)
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complement(172. .390)
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11903 ATCCGGATGCGAGCCACGCCACCACTA-
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GKSSFYWLTALAAUWHAGALMSGPILBEGGICUKRRNOVGVTLVIGATGTVACLIAGOIFGVG
AMIVRA PGAARFIARHVIOPABGGTLLDILLITLINGIAEBHFRGALYTALGRRYPY
TISTVIYVGATMASANIMIGFAAJIFVGTVCALERRASGGVLAPILTHFVWGLIMVFAI.
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/froduct "enoy! con hydrarase/isomerase lamily profein"
/frodein tal "AAASA 44.1"
/du.xtet-"di:\a880763"
/translation-"MSNYKIDTRTIVPGLAVTLADGVLSVTIDRPESIASLTKPVLAG
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PLOPVVAVVVOCPTVGGOSLALACIDEVLASDREFMLAHTVWGLMPDGGASA I VQAA
I GRI RAMHMA ILLPPVYPAALALISMGI VSAVY PAADFDAEVDK I SKILLAGIALI AKT
KNA I NAATL TELLAPTI LRELDGQALLLETDDFAEGATFRQQRRTPMFTGK
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EIJALKLIARADVLIEGYPRGYTERCIGDEEGAKVNRLIYARMTGWOOTGPRSQQAG
HID IN YISLNGILHAIGRGDERPVPPLNLVGDFGGSMFLLVGILAAIJMFRJSSQRGOV
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PUFYAAMLAGLGLDAAELPPQNDRAKWPELRALITEAFASHDRDHWGAVFANSIDACYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /hote-"similar to GB:U00096 PID:1742270 PID:1742276
PID:1787660; identified by sequence similarity; putative"
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/qene="MT1175"
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PID:1787660: identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                           /note-"identified by Glimmer2; putative"
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/gene-"MT1176"
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0; Mismatches
                                 complement(9272. .10771)
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complement(9272. .10771)
                                                                                                                                                                                                                                                                                                 Score 698;
                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                               50.18;
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Best 1 .cal Similarity 70.4
Matches 974; Conservative
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ATFWPRLAGACHTHRHTERAILDAGFVVDSSRREMAFPAMVPLPVSELALGREAHRT"
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COMPLEMENT (5008 . 5163)
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Agene="Whilito"."

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7872...8522

/gene="Whilso"
/gene="Whilso"
/gene="Whilso"
                                                                                                                 HMMH
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I (bases 1to 33100)

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Mycobacterium tuberculosis H37Rv complete genome; segment 87/162.
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Mycobacterium tuberculosis H37Rv
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Nature. 393 (6685), 537-544 (1998)
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Parkhill, J.
Direct Submission
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cubmilted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1806198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream codon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          penicillin binding proteins and eg DAC_STRSQ P15555 d-alanyl-d-alanine carboxypeptidase (406 aa), fasta srores, opt. 382,E(): 3.1e-17, (28.0% identity in 379 aa overlap); containsPS00013 Prokaryotic membrane lipoprotein /codon eter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Rv1923, (MTCY09F9.41c), len: 446 aa. Similar to esterases, beta-lactamases, eg G151214 esterase, (389 aa), fasta scores, opt: 569, E(): 5.4e-29, (33.7% identity in 401 aa overlap) also MTCY277.19 (56.6% identity in 410 aa
                                                                                                                                                                                                                                                                                                                                                                        Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //octe="PS00013 Prokaryotic membrane lipoprotein lipid
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                                                                                                                                                                                                                                                                                                                                                                                                                         available on the World Wide Web.
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265. .1380
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/gene="lipD"
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Acyl-CoA synthase similar to eg Y06J_MYCTU 010976
hypothetical 67.9 kd protein cy338.19 (626 aa), fasta
scores, opt: 945, E(): 0, (39.8% identity in 598 aa
overlap), also G1171128 SAFRAMYCIN MX1 SYNTHETARSE B(1770
aa), cpt: 845, E(): 0, (37.4% identity in 593 aa overlap)
also MTCY19G5.07 (36.9% identity in 590 aa overlap) similar to Rv3801c, (637 aa, 47.1% identity in 612 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aa. Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2748. .3128)
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3285. 5147
3285. 5147
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5871. 661
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gene

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/note="Rv1927, (MTCY09F9.37c), len: 257 aa, Slight similarity with YQJF_BACSU P54543 hypothetical 23.9 kd protein in glng- (209 aa), fasta scores, opt: 230, E(): 2.8e-08, (28.0% identity in 164 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement (6648. 7415)
/genew Rv1928c.
/note-"Rv1928c. (MTCY09F9.36), len: 255 aa. Similar to ellifa. ECOLI P25529 7 alpha-hydroxysteroid dehydrogenase (255 aa), fasta scores, opt: 541, E(): 1.2e-27, (37.5% identity in 251 aa overlap); also similar to many mycobacterial proteins, e.g M. tuberculosis Rv1350, kv0927c, Rv2002, Rv0769, Rv2766c, etc; contains PS00061 sinct-chain alcohol dehydrogenase family signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22248 CGCGGGTGCTCCATCTCAAGTGCGTTGACCACCCCGGAATTGCTGGCCTGTTTGC 22307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 aacgccagggcctgatcggcgaggcgcacgtcaaagtgattcgcgcctttttcgcccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1111 1111 11111 | 11111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
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IWTSAGTTANWIFLLARTDPSAAKHRGLSFLLVPMDOPGVVRPIVNAAGHSSFSEVF
LTDARTSAGNVVGRVGDGWSFAMTLLGFERGSHIATAAIDFERDLORLCELARDRGLH
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VEILGLEALGPRGPGNGGRRLVPEAGTPNSPACWMDELLYARAATIYAGSSQIQRNVI
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HWRRALAGACLVAVSWPTEYXGGCLSPMEQVVLAEEFARAGAPERAENDLFGIDLLGN
TLIALGSEAOKRHFLPRILSGEHRWCQGFSEPEAGSDLASVRTRGVLDGDEWYINGHK
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VIJDVARVLIJAAEMLGGAEACLDLAVOYAGERROPEDRPIGSFOAVKHACADMMI EIDAT
KATVMPAAMSAANGDELGTVAPLAKAQTAETFVLCAGSALQ I HGATAFTWEHDLHLYY
KKAKTTEALFGSSARNRALLAERAGLVKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"mdp-kystequdp-raslercercapyremaadgesdrrewqrlc
telelipaliyippen gelgatevera faraelgralptp-praatyfatealeralbrodeg
kkrillagilitgar i gittavsghdyasattyraykrdgepalitgecttyvlhghya<u>b</u>efy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAQITLEGNAINTVGELPAVGSPAPAFTLTGGDLGVISSDQFRG
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          Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Mill, J., Mikula, A. and Bishai, W. Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
                                                                                                                                                                                                                                                                                                                                                                                   9712
                                                                                                                                                          Outpublished

Chases I to 14179)

Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Ernolaeva, M., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ernolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Biller, A. Mikula, A. and Bishai, W.

Direct Submission

Submitted (25-APR-2001) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Increasing/Qualifiers

1. .14179
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condition (1678. .2907)

condition (1678. .2907)

condition (168.x61931 PID:47382; identified by /note="similar to GB:x61931 PID:47382; identified by
Utterback, T., Weidman, J., Khouri, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"similar to GB:U00096 PID:1742169 PID:1742181
PID:1787584 PID:1931625; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ordiname_Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
/db_xref="taxon:83331"
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/protein_id="AAK46255.1"
/db_xref="G1:13881641"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="thiol peroxidase"
/protein_id="AAK46254.1"
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/gene="MT1984"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="clinical strain"
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91. .588
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TQQEAPEETRILLIDFLGGIRP"
TQBAB13...9328
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8813...9328
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DVI RAGPLCMAEGARLKDAFVYPETMPAWFTEADLDFYTGEFERSGFGGPLSFYHNID
                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MSCTFDMVPFTYDHIDEVGLRRVFGCFPCGVJAVCAMVDDQPVG
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AAAASATSVAADIVURVORVOQAQBOCVLGRRAGABANDLARLAERERAALICETV
SIVDRVQMAHAHAESVERAVEHGLAMVSIGELVAYRRR ERQVVRFTAATI.PTWAGASR
VIGFRUVYDLGEHI.AVIVGAVGAGVPVPLHVHIECLTGDVFGSTACRCGEELNGALAR
                             HQIPALAGAGYRVVAIDQRGYGRSSKYRVQKAYRIKELVGDVVGVLDSYGAEQAFVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /hote-"similar to GB:L09228 SP:P17620 GB:X51510 P1D:40087 P1D:410127; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13009 ACCCCCCCCCCTGACCGCTGAACCCTGCCAGCGCAGTTGACCGCGCCCCCCCTC 13068
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                                                                                                                                                                                                                                                                /hote-"similar to GB:X63449 P1D:46811 SP:002058; identified by sequence similarity; putative" /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14179;
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Pred. No. 2.6e-84;
0; Mismatches 395; Indels
                                                                                                                                                                                                                                                                                                                                                          /product-"dimerase, putalive"
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9325. .10386
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/qene-"MT1989"
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Matches 964; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGRGECEFIIRLLPDGVWSNYLRDRAQPGDHIALKCSKGSFYLRFIVKPVILVAGGTG
LSATLAMAGSLDADVAHPVLLYGVERTEDLCLETERRRGVGRLEHVVVARGTG
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LGGTWRKPGTSDIE IVCAGRELLEWVYRRLLDDERNIDFRYSSEVADIAFDRANNAIV
GVAVDNGDADGGDGLQVVPAEFVVDASGKNTRVPFFLERLGVGAPEAEQDIINCFYST
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RERRAFADLWRSPVIGENIDGLEPASPIYNRRYPMLRLRYEKKRULPRALLAVGDAY
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IASRVLGKWARTRLSGQKTLIARNYENHPIPAEPADQLVNA"
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VTGDGVVTAVELVSPSTAILRVDTSGMAGALRYRAGQFAQIJQVPGTNVWRNYSYAHPA
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                                                                                            protein family HMM
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/product="enoyl-CoA hydratase/isomerase
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/protein_id="AAK46260.1"
                                                                                            by match
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/db_xref="G1:13881645"
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/note="similar to
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/103. 5212
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DNA encoding an ac LigAT2 domain from Human colon cancer

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BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
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/note= "BCG delta l deletion region"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Score 1202.4

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Post-processing:

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Total number of

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Scoring table:

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This DNA sequence comprises Mycobacterium bovis BCG deletion
sequence BCGdelta3. A specific genetic deletion of this region
ceaults in an avivalence phenotype of the mycobacterium. 2 other
celetion regions (see AA713535 and AA73535) have also been detected.
Identification involved screening a BCG cosmid library with a
redicible deprobe obtained following DNA subtraction between
virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.
The deletions provide useful markers for the identification of an
avirulent, or a virulent, mycobacterial phenotype. Determination
of avirulence requires the detection of the presence or absence of
the deletion; the deletions are detected either by detecting the
presence or absence of deletion junctions (see AA733538-46), or by
detecting the presence or absence of the sequences contained within
the deletion. Deletion polypeptides are used as components of
Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
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                                                                                                      Example 1; Fig 3; 66pp;
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Length 12412;
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                   51; Indels
Score 1202.4; DB 17;
Pred. No. 5e-212;
                   0; Mismatches
 86.3%;
                     Conservative
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Matches 1290;
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M. tuberculosis cellular uptake gene region.
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                 The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. Wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydroj hobic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with list carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAR71931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 acctuaccgacaccgaacgcgcccgcaaacgcggcatcaccctqagcaaccaqcaac
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                                                                                           DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                       Length 1535;
                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                        Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                     Query Match
32.7%; Score 455; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.1e-75;
Matches 455; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           794 acgacgggctgctggccgggctgcgcgcgctgatc 828
                                                                                                                                  Claim 2; Page 9-11; 46pp; English.
                           (CORR ) CORNELL RES FOUND INC
         93US-0118442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT33656 standard; DNA; 1535
                                                                WPI; 1995-115442/15.
P-PSDB; AAR71931.
         02-SEP-1993;
                                              Riley LW;
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A DNA molecule (AAT3165b) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophages. The encoded protein sequence is given in AAM02301. The DNA was obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript II vector and screening recombinant E. coli strains for HeLa cellminsus colores. The DNA includes 2 separate coding regions (see also AAT31657-58) confine for the cell entry (AAM02302) and macrophage survival (AAM02301) proteins. He can be used to produce the cellular uptake proteins used as vaccines of to facilitate uptake of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 galoggogaygogrargloaaaqi.gatloyogooottiltogoooacetgooogoogg 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycohacterium tuberculosis infection
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Cellular uptake; cell entry; macrophage; passive immunisation;
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                                                                                                                                                                                                                                                                                                              protein
                                                                      tuberculosis strain H37Ra (ATCC 25177).
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                                                                                                                                                                                                                                                                                                       /product= macrophage survival
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/label- ORF-1
/product= cell e
886..1535
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/label- ORF-2
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                             gene therapy; ds.
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                                                                      Mycobacterium
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                             vaccine;
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(first entry)

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                                                                                       to enhance uptake of in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within macrophages. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to
                                           acaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaacc
                                tgctagccaaactggccgcccccggcgcgaccaaccccgacgaccacaccccggtcatcg
tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                   DNA for M. tuberculosis cellular uptake protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis DNA - confers ability therapeutic agents e.g. antibiotics, also useful
                                                                                                                                                                                                                                                                                           Cellular uptake protein; vaccine; infection; ds
                                                                                                                                   /note= "stop codon not given"
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                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protect
                              tgctagccaaactyyccyccccqqcycqacraacccgacgacacacccggtcatcy
                                                            tgctagccaaactuqccgcccccgycqcqaccaaccccgaccacaccccggtcatcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to p mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                macrophage survival; vaccine;
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Indels

0; Mismatches Score 455; Pred. No.

Length 1535;

DB 19; 4.1e-75; ; 0

32.7%; 100.0%;

Query Match 32.7 Best Local Similarity 100. Matches 455; Conservative

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                                                                                                                                                                                                                                                                                                                         II vector and screening recombinant E. coli strains for HeLa cell-invasive clones. It can be incorporated into a vector and used for prodn. of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g., therapeutic genes, into mammalian cells. A second DNA molecule (AAA13657) codes for a protein (AAM01302) that confers on M. tuberculosis the ability to enter mammalian cells.
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                                                                                                                   Gaps
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0
                                                                                                 Length 650;
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                                                                      BP; 123 A; 258 C; 185 G; 84 T; 0 other;
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                                                                                               Score 396; DB 17;
Pred. No. 2.6e-64;
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/note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; infection;
                                                                                               28.4%; Score 396; DE i urity 100.0%; Pred. No. 2.6 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                               AAV18649 standard; DNA; 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0689411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cellular uptake protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...649
                                                                                                       Simi arity
                                                                      Sequence 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9805784-A1
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                                                                                                                396;
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                                                                                                Query Match
Best Local S
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enhance uptake of
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                                                                                                                                                                                              The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which conters on M. tuberculosis an ability to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DNA fragments or anti-reoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gaceteaceqacarryaangegreegraaaegeggcateaceetgagcaaceageaatae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                          vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                       i to
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 650 HP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                     um tuberculosis DNA - confers ability agents e.g. antibiotics, also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 396; DB 19;
Pred. No. 2.6e-64;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 14; 82pp; English.
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100.0%;
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                                                                                                     Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 396; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces avermitilis.
                                      WPI; 1998-145620/13.
Riley LW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agrochemical; ds.
                                                           P-PSDB; AAW47543
                                                                                                                      therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avermectin aglycone synthase DNA and proteins encoded by all or part of it for the production of avermectin and its derivatives for drug and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21482 gatacaccetegeceaegecegegegegtgttegaceaeegegeeaeeeteategeegeeg 21541
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Location/Qualifiers
1.11919
/*tags a //tote avermectin aglycon synthase protein"
11971..30690
                                                                                                                                                                                                /*tag~ b
/note= "avermectin aglycon synthase protein"
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illarity 45.0%; Pred. No. 5.2e-09;
Conservative 0; Mismatches 631;
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detection; mapping; tissue typing; profiling; forensic; cancer;
genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynuclectide sequences given in AAZ1233 to AAZ17779. The polynuclectides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profilling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynuclectides and be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynuclectides may also be used to construct arrays for diagnostics (which may be used to determine function of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). "he polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                               Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Gises K, Innis MA;
Jones WL, Kasam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human genes and their expression products which are differentially expressed in different cell types
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1 Garcia PD,
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                    05-AUG-1999
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5; gacgocgcccggcgcatcgccgacgccgatctcggacctcgtcgagcactcaccggt 320 gaggogcacgtcaaagtgattcgcgccctttttcgcccacctgcccgccgcggtggatgt 440 cgagetggcccgctacgcccagcgggtcatggactggctacaccccgacggcgacctcac 560 gaaccgctagccccacagttgaccgccaccgccccaacgccagggcctgatcggc gtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatatcgtcccga 11; 6.4%; Score 89.8; DB 20; Length 1337; 23.4%; Pred. No. 3.3e-08; ive 0; Mismatches 860; Indels 11; Conservative Query Match Best Local Similarity Matches 266; Conserv 166 226 381 321 286 501 q g g δ ò ò

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                                                                                                                                                                                                                                                                         Mutated Type I polyketide synthase containing a extension module for replacement of a reductive producing polyketides, e.g. Bl avermectin
                                                                                                                                                                                               Staunton J,
                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7a-f; 75pp; English
                                                                                                                                               (BIOT-) BIOTICA TECHNOLOGY LTD
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                                                                                99WO-GB02158
                                                                                                               98GB-0014622
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               WO200001827-A2
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Streptomyces hygroscopicus
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9048

8989 catcaccccactactacgccggacactccctcggcgaaatcaccgccgccactcgc

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714 cgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgaccgcgacaccc

774 cagecaageccaacgcaaccacgacgggetgetggeegggetgeggegegetgategenete

eggeatecteaceteacegaegecaceaceteateaceaaegegecaceteatgea

The prescut sequence represents an NheII-XhoII fragment that encodes module 8 of te FK-520 polyketide synthase (PKS) gene cluster with the endoqueous acyltransferase (AT) domain replaced by the AT domain of endogenous acyltransferase (AT) domain replaced by the AT domain of module 12 of the rapamycin PKS (which is specific for malonyl CoA).

FK-506 is a potent immunosuppressants, and acts through intial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide compounds. The polyketide compounds can be used as immunosuppressants to prevent or treat transplant rejection, graft-versus-host disease or uveitis. They can also be used for treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease, multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurons in the outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and control of the brain. They can also be used for treating e.g. Parkinson's disease, also be used for treating e.g. Parkinson's disease, better the prain inplury, or peripheral neuropathies. They can also be used in agricultural and control of the prain in a proper prop New isolated polyketide synthase nucleic acid and polyketide compounds, useful for treating e.g. transplant rejection, uveitis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or Wu K; ů, Example 1; Page 82-85; 126pp; English. Santi BIOSCIENCES INC 99US-0102748. 99US-0123810. 99US-0139650. Chu D, Khosla C, peripheral neuropathy WPI; 2000-317716/27. P-PSDB; AAY84727 (KOSA-) KOSAN 11-MAR-1999; 17-JUN-1999; Reeves C,

Sequence 4466 BP; 634 A; 1796 C; 1433 G; 603 T; 0 other;

veterinary applications.

; 3784 3605 gcaacaccacctcaccaccaccgaccacacctcatcgtccacaccaccaccgacccgc 3664 catggccgatgtgatccgcatgaccagccacgccaccactactcccccgcaagcgggag 1007 gtacccccaggcgatcttcgaccacggcacaccctggcgctgtatcacaccaaacgcct 1067 3545 cgaccccgaggacatacccaccgcgcccacacccgcgcccacccgcgtcctgaccgcct 3604 agecteceggeceagegateatgetgttegecaaegaeegeggetgeaeeaaaeeegg 1127 caccaccacccaccaccaccacccccctcaaccccgaacacgccatcatcatcaccgq 3904 1188 acgcaccgacatcaccgagctgaccctggcctgcggccccgacaaccgactcgccgaaaa 1247 egectecgggaaactgggccaacacaacggtettecegtetegategtggteaceacae 887 3725 cctcategaaaccgaccacacacccccctcccctggcccaactcgccacctcga 3665 eggegecacegicaceggecteacegeacegeceagaacgaacaceceacegeateeg cctgaccgacctgcaaaccggcgccggcaagggcttcaccggcggcggcaccctgctacc 1128 ctgtgacgcaccggcctaccacagccaagcccaccacgtcaccgcctggaccagcaccgg 0; Score 87.4; DB 21; Length 4466; Pred. No. 9.5e-08; Indels Mismatches 296; .. 6.3%; ilarity 47.2%; Conservative (Ouery Match Best Local Similarity Matches 265; Conserv 828 888 948 1008 1068 3845 g ò d ŏ QQ Š a δ g

3905 eggetecggeacetegeeggeatectegecegecacetgaaceaceceacacetace 3964 immunophilin; FK-506 binding protein; polyetide compound; uveitis; transplant rejection; qraft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss. cototocoggaecocaccocogaegaegaececeggeaeceaectococtgegaeulegg gene cluster; immunosuppressant; Nucleotide sequence of a fragment of the FK-520 PKS gene cluster. polyketide synthase; PKS; 1368 agacgacgacgacaaacccga 1388 ΗБ 4085 ccacacegeegeeacetega 4105 AAA14661 standard; DNA; 4478 (first entry) 08-AUG-2000 Synthetic AAA14661; 1308 AAA1466. a à ò

/*tag= a /mote= "no termination codon given" Location/Qualifiers Streptomyces hygroscopicus 3..4466

98US 0102748. 99US-0123810. 99US-0139650. 99WO US22886 WO200020601-A2. 01-OCT-1999; 02-0CT-1998; 17-JUN-1999; 1.1-MAR-1999; 13-APR-2000

Santi D, Chu D, Khosla C, WPI; 2000-317716/27. Reeves C,

(KOSA-) KOSAN BIOSCIENCES INC

Wu K;

New isolated polyketide synthase nucleic acid and polyketide compounds, useful for treating e.g. transplant rejection, uveitis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or peripheral neuropathy P-PSDB; AAY84725

Example 1; Page 76-79; 126pp; English.

The present sequence represents an AvrII-XhoII fragment that encodes module 8 of te FK-520 polyketide synthase (PKS) gene cluster with the endogenous acyltransferase (AT) domain replaced by the AT domain of module 12 of the rapamycin PKS (which is specific for malonyl units). FK-506 is a potent immunosuppressants, and acts through intial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide

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be used as immunosuppressants to
                             uveitis. They can also be used for treating e.g. alopecia universalis, autoimmune chronic active hepatitis, inflammatory bowel disease, multiple sclerosis, primary biliary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurite outgrowth in NGF-treated Poll cells and in sensory neuronal cultures, and in intact animals, they promote regrowth of damaged facial and sciatic nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
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                       prevent or treat transplant rejection, graft-versus-host disease or
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Pred. No. 9.5e-08;
O; Mismatches 296;
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  The polyketide compounds
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Matches 265; Conserv
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module 8 of the FK-520 polyectics an international regions. The product of the repeated of the FK-520 polyectics of FKS) gene cluster with the cudogenous acyltranslerase (AT) domain replaced by the AT domain of module 13 of the repanying the FK by the AT domain of FK-506 is a potent immunosuppressure; and acts through infal formation of an intermediate complex with protein immunosphilins known as FK-506 binding proteins. The moticie acids are used for producing professure in the moticie acids are used for producing professure to prevent or treat transplant rejection, graft-versus-host disease or uveitis. The polyketide compounds can be used as immunosuppressants to prevent or treat transplant rejection, graft-versus-host disease or uveitis. The bolyketide compounds can sobe used for inversalis, multiple sclerosis, primary billary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurine cuttree had in intact animals, they promote regrowth of damaged facial and scient nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheiner's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
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immunophilin; FK-506 binding protein; polyketide compound; uveitis; transplant rejection; graft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss.
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9-14535
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17-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunophilin, FK-506 binding protein; polyketide compound; uveitis; transplant rejection; graft-versus-host disease; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary bilary cirrhosis; scleroderma; neurite outgrowth, nerve regrowth, Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
                                                                                                                                                                                   1188 acgcaccgacatcaccgagctgaccctgggcctgcggcccgacaaccgactcgccgaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1248 aggetggaccaccacaacaacaccacggccacaccgaatggetaccaccacccacct
                                                                    catggccgatgtgatccgcatgaccagccacgcccactactcccccgcaagcgggag
                                                                                                                                                         1008 gtacccccaggcgatcttcgaccacggcacacccctggcgctgtatcacaccaaacgcct
                                                                                                                                                                                                                                                   agectecceggeceageggateatgetgttegecaacgacegeggetgeaccaaaccegg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgaccacggccaacccgcaccaaccattccaccacccgaacgattcctccacaacca
                                                                                                               cygcyccaccytcaccygcctcacccyccccayaacyaacaccccaccycatccy
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/note= "no termination codon given"
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/*tag= a
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99US-0123810.
99US-0139650.
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11-MAR-1999;
17-JUN-1999;
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module 8 of the FK-520 polykeines an AVIII ANOII Inguinel Lifet which the endogenous acyltransferase (AT) domain replaced by the AT domain of endogenous acyltransferase (AT) domain replaced by the AT domain of module 13 of the rapamycoin PKS (which is specific for methylmalonyl CoA). FK-506 is a potent immunosuppressants, and acts through intial formation of an intermediate complex with protein immunophilins known as FK-506 binding proteins. The nucleic acids are used for producing polyketide compounds can be used as immunosuppressants to prevent or treat transplant rejection, graft-versus-host disease or uveitis. They can also be used for treating e.g. alopecia universalis, multiple sclerosis, primary bilary cirrhosis, or scleroderma. They also have neurotrophic activity and can be used to promote neurite outgrowth in NGF-treated PCI2 cells and in sensory neuronal cultures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and in intact animals, they promote regrowth of damaged facial and sciatic nerves, and repair lesioned serotonin and dopamine neurons in the brain. They can also be used for treating e.g. Parkinson's disease, Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or peripheral neuropathies. They can also be used in agricultural and
                                                                                                                                                                                                                            New isolated polyketide synthase nucleic acid and polyketide compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents an AvrII-XhoII fragment that encodes
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                                                                                                                                                                                                                                                               useful for treating e.g. transplant rejection, uveitis, multiple sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4571 BP; 659 A; 1829 C; 1469 G; 614 T; 0 other;
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Pred. No. 9.5e-08;
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(KOSA-) KOSAN BIOSCIENCES INC
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                                                           Khosla C,
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es 265; Conserv
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                                                           Reeves C,
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Matches
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/note= "acyltransferase domain (AT) 6"
complement (17820..19053)
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/note- "dehydratase domain (DH) 6"
complement (16587..17820)
                          complement (13761..14394)
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/note= "ACP5"
complement (19464..20097)
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/note= "DH5"
complement (21420..22653)
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/note= "fkbB_gene"
complement (24163..24373)
                                                               complement (14517..15294)
                                                                                                  complement (15438..16587)
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/note= "DH4 (inactive)"
complement (26146..27430)
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/*tag= af
/note= "DH3 (inactive)"
complement (31018.32185)
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/*tag= ah
/note= "KS3"
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/note* "DH2 (inactive)"
 /*tag= n
/note= "ACP6"
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/note= "ACP4"
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/note= "ACP3"
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/note= "AT4"
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/note= "KR3"
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/note= "AT3"
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FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; Streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveitis; alopecia universalis; autoimmune chronic active hepatitis; inflammatory bowel disease; neultiple solerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease; Alzheimer's disease; stroke; traumatic spinal cord; brain injury; peripheral neuropathy; ss.
                                                                                                                                                                                                                    Nucleotide sequence of the FK-520 biosynthetic gene cluster.
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                                                                                                                                           AAA14651 standard; DNA; 77536 BP
                                                                     1368 agacgacgacgacaaacccga 1388
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61220 cgaccccgaggacatacccacccgcgcccacacccgcgccacccgcgtcctgaccgcct 61279
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                                                                                                                                                                                                                                                                                                                                                                                                                       61580 cggctccggcacctcgccgcatcctcgccgccacctgaaccaccccacct 61639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catggccgatgtgatucgcatgaccaccaccactactccccgcaagcgggay 1007
                                                                                                                                                                                                                                                           1068 agcolococqqcccaqqqqtvalqctqltcqccaacqacqcqqqqtqccaaaccqqq 1127
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                                              888 cctgaccgacctgcaaaccggcgcgcggcaggggttcaccggcggcggcaccctgctacr 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis; multifunctional enzyme; polyketide; avermectin; veterinary drug; agrochemical; ds.
                                                                                                                                                                                      1008 glaccccuagucgalettegaecaecggeacaecectggegetgtateacaecaaaegeet
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1..14646
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/*Lay= al/21424...31422
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/*tag= b
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Best Local Similarity 47.2%; Pred. No. 1e-07;
Matches 265; Conservative 0; Mismatches 296; Indels 0;
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                                                                                                          somplement (38371..38581)
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99JP-0046961.

4-FEB-1999;

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(KITA) KITASATO INST

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The present sequence represents DNA which encodes avermectin aglycon synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA; (2) expression vectors containing the DNA; (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformants; (5) preparation of avermectin aglycon or its derivatives by culture of transformed evermectin-producing microorganisms; and (6) oligonucleotides of 5-60 bases in length containing sense or antisense sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified forms of avermectin and of the intermediates in its blosynthesis, for use as drugs, veterinary drugs and agrochemicals.
                                                                                                             Avermectin aglycone synthase DNA and proteins encoded by all or part it for the production of avermectin and its derivatives for drug and
                                                                                                                                                                                                    Claim 2; Page 134-203; 314pp; Japanese
                                                                 P-PSDB; AAB23751, AAB23752
                                           WPI; 2000-565458/52
  Ikeda H;
                                                                                                                                                             agrochemical use
  Omura S,
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21; Length 31422; Indels Score 86.6; DB 21; Pred. No. 1.4e-07; 0; Mismatches 489; .4e-07 6.2%; Best Local Similarity 46.9 Matches 451; Conservative Local Similarity Ouery Match

Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;

22:47:50

2, 2002,

Search completed: April Job time: 9130 sec

5 22152 cacceaeccegtettegoeg@cgcacteaacgacatetgeaeceaectegaececeaect 22211 22332 ccaygicgcctccacc--gcctcctcaccgacggctaccacatcaccrccartartar 22389 22569 egacetegecategeegecateaacacececacetecetegeateageggeacececea 22628 22629 caccgiccaacacaicaccaccititgccaacaacaaggcaicaaaaaccaaaacciicc 22688 743 504 getggecegetaegeceagegggteatggaetggetaeaeceegaeggegaeeteaeega 563 caccegecaggeegeegaageegaectggeeggeaageegeteaatategteeegaega 503 854 caccgaacgcgccacaaacgcggcatcacctgagcaaccagcaatacgacggcatgtc acggctaagtggctacctgacccccaagcgcgggccacctttgaagccgtgctagccaa actggcgccccgggggggacaacccgacgacgacgacaccccggtcatruacarrarer gccggacactccctcggcga-aatcaccgccgccacctcgccggcatcctcaccvt.cac 855 cggtcttcccgtctcgatcgtggtcaccaccac----cctgaccgacctgcaaaccgg cyccygcaagggcttcaccggcggcggcaccctgctacccatggccgatgtgatccgcat gctggccgggctgcgcg-----ctgatcgcctccgggaaactgggccaacaca 969 gaccagccacgcccactactccccgcaagcgggaggtacccccaggcgatcttcga 444 624 684 744 564 22272 22212 22390 804 606 g δ δ qq QQ ò ò ò g q οy δ g ò g ò g ò

chaeggeacaccetggegetgtateacaccaaacgeetageeteceeggeecagey

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22689 caccaaccacgccttccactccaccacaccaactccaccagra

catgotyltogccaacgaccgcggrtgcaccaaacccggctgtgacgcaccggcctacca 1148 1206 getgaccrtggcctucggcccrqaraaccgartcgccqaaaaaggctggaccaccracaa 1149 cagrecaagrecarrungleacegrelygareageaceggacaterrunenga caacacccacggcranaccgaatggclaccarcacccracctcgaccacggccaacccn caccaacactteraccaccegaangaltectecaccaagacgacgacgaraaace c 23109 1386 c 1386 1266 1326 23109 a ŏ qq q à ŏ ŏ q ŏλ

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                                                                                             Sequence 3, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 18, Sequence 3, A Sequence 3, A Sequence 3, A
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Sequence 4,
                                                    Sequence 2,
Sequence 2,
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Pred. No. 1e-266;
0; Mismatches 21; Indels
US-07-951-715A-2
US-08-459-448A-2
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US-08-387-942C-1
US-08-459-448A-3
US-08-459-4448-3
US-08-459-504B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHYER, Owen R.
APPLICANT: VEYERS, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
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98.4%;
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US-09-103-840A-1/c
Query Match
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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      Db
      1789467 AGGCCTGATCGCCGACGCACGTCAAAGTGATTCGCCCCCTTTTTCGCCCACCTGCCC
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Db 1789227 C...nav.cacGcanfctacGgcradTGGCTACCTGACCCCCAAGCGGCATGTCTT 1789168
                                                                                                                                                                                                                                   1789347 CAATATCGTCCCGACGAGCTGGCCCGCTACGCCCAGCGGGTCATGGACTGGCTACACCCC 1789288

        QY
        547 gacggcgacctcaccgacaccgaaacgcgcccgcaaacgcggcatcaccctgagcaaccag 606

        Db 1789287 GACGGCCCCACACCGACACCGCACACGCGCCAAACGCGGCATCACCCTGAGCAACCAG 1789228

1789527 GAGCACTCACCGGTGAACCGCTAGCCCCACAGTTGACCGCCACCGCCCACCGCCCAACGCC 1789468
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        907 gacgccggcaaggcttcaccggcggcggcaccctgctaccatggccgatgtgatccgc 966

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        1788927 GGCGCGGCGAAGGGCTTCACCGGCGGCGCGCCTGCTACCCATGGCCATGTCATCGCC 1788868

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RESULT 2 US-08-390-878-18

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Sequence 18, Application US/08390878
Patent No. 5700683
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS NUMBER OF SEQUENCES: 18
                                                                                                                                     Crew
20th
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                                                                                                                                            ADDRESSEE: Townsend and Townsend Khourie and Cre
STREET: One Market Plaza, Steuart Street Tower,
                                                                                                                                                                                                                                                                                                                                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
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Pred. No. 3.3e-246;
0; Mismatches 51;
                                                                                                                                                                                                                                                         COMPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: HULter, Tom
REGISTRATION NUMBER: 498
REFERENCE/DOCKET NUMBER: 155
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-390-878-18
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95.78;
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 415/543/5043
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                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              CITY: San Francisco
STATE: California
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                                                      cacctttgaagccgtgctagccaaactggccgccccggcgcgaccaaccccgacgacca
                                                                                                     Sequence 1, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses
                                                                                                                                                                                                                                             gatecgeatgaceageceaceceacetactececegeaageggaggtaceceagge
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US-08-464-052-1
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                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.7%; Score 455; DB 3;
100.0%; Pred. No. 3.9e-88;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             (D-1485B)
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                                                                                                                                                                                                                                             NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    APPLICATION NUMBER: US/08/464,052 FILING DATE:
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HW PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                     TELEPHONE: (716) 263-1304
TELEPAX: (716) 263-1600
INFORMATION FOR SEQ 10 NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1535 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  unknown
SEQUENCES:
                                    STREET: Clinton
CITY: Rochester
                                                                STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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TOPOLOGY: un
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Best Local $
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ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
CTTY: Rochester STATE: New York
          1247 ACGACGGCTGCTGGCCGGGCTGCGCGCGCTGATC 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19603/187
                                                                                                              . Sequence 1, Application US/08689411
; Patent No. 6224881
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
APPLICANT: Chong, Pele
TITLE OF INVENTION: CELLULAR UP
TITLE OF INVENTION: CELLULAR UP
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
US-08-689-411-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 14603
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                                                                          RESULT 5
US-08-689-411-1
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Sequence 1, Application US/08461002
Patent No. 6214543
GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.7%; Score 455; DB 4; 100.0%; Pred. No. 3.9e-88; tive 0; Mismatches 0;
                                                                                                                                   ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acgacgggctgctggccgggctgcgcgctgatc 828
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/461,002
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                   ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.79
Best Local Similarity 100.
Matches 455; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-461-002-1
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DNA MOLECULE FRAGMENTS ENCODING FOR
CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES
THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%: Score 455; DB 4; Length 15: 100.0%: Pred. No. 3.5e-88; O. Mismatches 0; Indels
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION 194PA:
APPLICATION NUMBER: US/08/689,411
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1127 TGCTAGCCAAACTGGCCGCCCCGGGGGGGACCAACCCGGACCACACCCCGGTCATGG 1186
                                      494 gicccgacgagctggcccgctacgcccagcgggicatggactggctacaccccgacggcg 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 455; DB 5; Length 1535; 100.0%; Pred. No. 3.9e-88; Live 0; Mismatches 0; Indels
                                                                                                                                                                                      Sequence 1, Application PC/TUS9409863
GENERAL INFORMATION:
APPLICANT: Riley, Lee W.
TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR
TITLE OF INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMan Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELEFAX: (716,263-1000
TELEFAX: (716,263-1600
TELEFAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE :HARACTERISTICS:
LENGTH: 1555 base pairs
                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COEMTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                         ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09863
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PCT-US94-09863-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                                             New York
: U.S.A.
                                                                                                                                                                          PCT-US94-09863-1
                                                                                                                                                                                                                                                                                                               CITY: ROC
STATE: NE
COUNTRY:
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Best Local S
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GENERAL INFORMATION:
APPLICANT: Kiley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
gacctcaccgacaccgaacgcgccagcaaacgcggcatcaccctgagcaaccagcaatac 612
                                                             tgctagccaaactggcccccggcgcgaccaacccggacgaccacacccggtcatcg
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: 1BM PC computible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/08464052
; Patent No. 6008201
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TELLEFAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 5:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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: New York
RY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396;
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Best Local S
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DNA MOLECULE FRAGMENTS ENCODING FOR CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
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No. 1e-75; 0; 7
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SOFTWAKE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/UN/AND/411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. le-
ive 0; Mismatches
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SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6224881
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REGIETRATION NUMBER: 30,727
REFERENCE/JOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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(716) 263-1600
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nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 396; Conservative
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TITLE OF INVENTION: CELL
TITLE OF INVENTION: THE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 1
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CITY: Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14603
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION UNBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 396; DB 4;
Pred. No. 1e-75;
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.4%; Scor. 100.0%; Pred. No. 10.00%; Pred. No.
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Patent No. 6214543
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US-08-461-002-5
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STATE: New York
COUNTRY: U.S.A.
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0; Mismatches 20
                                                                                                                                                                                                                             Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASEN, Claime M.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN, TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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COTHER INFORMATION: "n" bases at
COTHER INFORMATION: represent a,
CS-09-103-8408-2
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Best Local Similarity 98.5%;
Matches 1327; Conservative
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3869656 ggttacgcatcaccaagcccgacgccctacgcatcgccgacgccgatctcggac 3869715
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                                                                                       541 caccccgacygcyacctcaccgacacgacgcgcccgcaaacgcggcatcaccctgagc 600
                                                                                                         661 acctttgaagccgtgctagccaactggccgccccggcgcgaccaaccccgacgaccac 7:3870076 acctttgaagccgtgctagccaaactggccgccccgggcggaccacccgacgaccac
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      181 ttgacgcccaagccagcgaggaactgggcggcacqctqtgctgcgcgcgcgacc
      240

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      3883702 ttgacgcccaagccaggcgaggaagaactgggcggcggcgctgtgctgcgcgctgtgctgcgcgctgtccaacc
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                                                                                                                                                                        FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 1.3e-12;
tive 0; Mismatches 0;
                                                                                                                        APPLICANT: WHITE, Owen K.
APPLICANT: WHITE, Owen K.
APPLICANT: WENGER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
   ccgtggacctgtgagatacactacacc 3870762
                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                   Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                  Ö.
                                                                                              GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 1393; Conservative
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                                       RESULT 11
US-09-103-840A-1
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3884302 gcccaacgcaarrucgarggclyclyclyggctqrqcgcgctgatcgcctccvqggaa 3884361
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                          841 ctgggccaaracaarggtcttcrrgtrringatcgtggtcaccaccacctgaccgacctq 900
661 acctttgaagccgtgctagccaaactggccgccccggcgcgaccaacccgacgaccac
                                                                                     781 geocaacgeaacracgaeggetturigeegggetgegegetgategeteeggaaa
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Db 1780705 CGAATAGCCGGGAGGAGTTGTCGAGGTCTTTGATGCGCTGGATGCCGAGCTGGACCGCT 1780646
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                                                                                           Length 4403765,
                                      positions throughout 9
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                                                                                        Score 78.4; DB 4;
Pred. No. 8.9e-08;
0; Mismatches 39;
                                          various
t, c or
TYPE: DNA
CRGANISM: Mycobacterium tuberculosis
FEATURE:
CHER INFORMATION: CDC 1551
CHER INFORMATION: "n" bases at varid
CHER INFORMATION: represent a, t, c
US-09-103-840A-2
                                                                                        Similarity 97.2%;
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Best Local Simi
Matches 1344;
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Db 1779685 GACCACGCACACCCTGGCGCTATCACACACACACACACGCCTAGCCTCCCGGCCCAGCGG 1779626
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Sequence 2, Application US/09130114

Sequence 2, Application US/09130114

Sequence 2, Application US/09130114

Sequence 3, Sequence 2, Application US/09130114

Septicant Norman Sequence 3, Septicant Sequence 3, APPLICANT: Bombins, Alan K.

TITLE OF INVENTION: From Multiple Translected Episomes TITLE OF INVENTION: From Multiple Translected Episomes TITLE OF INVENTION: From Multiple Translected Episomes CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 43.1
Matches 342; Conservative
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; ORGANISM: EBNA
US-09-130-114-2
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1058 ccaaacycctaycctccccggcccagcgatcatyctyttcgccaacgaccqcgyctgca 1117
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378 tectectecegtectegtectectecegtectecegtectecegtectetegtecte 437
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                                       ccaaacccggctgtgacgcaccggcctaccacagccaagcccaccacgtcaccgcctgga
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APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaoan
APPLICANT: Perceda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: 1111nois
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08858003
Patent No. 6060234
GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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509 cccgctacgcccaqcggtcatggactggctacaccccgacggcgacctcaccgacaccq 568
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Pred. No. 1.2e-06;
D; Mismatches 275; Indels
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                                                                                                                 NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEFAX: (847)-938-2623
            MABER: US/08/858,003
16-MAY-1979
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Sequence 1, Application US/09078166

Patent No. 6063561

GENERAL INFORMATION:

APPLICANT: Staz, Leonard

APPLICANT: Stassi, Diane L.

APPLICANT: Summers Jr., Richard G.
                                                                                                                                                                                                                                                                                                                                                                                  0;
             APPLICATION NUMBER: US/08/
FILING DATE: 16 MAY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casulo
                                                                                                                                                                                                                                                                                                                                                      5.0%;
                                                                                                                                                                                                                                                  : 925 base pairs
nucleic acid
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-858-003-1
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STRANDEDNESS:
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                           APPLICANT: KAKATAS, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 925;
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                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWALE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,166
FILING DATE: 16-MAY-1979
CLASSIFICATION:
PROR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REFERNICE/DOCKET NUBBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
                                                                                                                         ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Rd.
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
Ruan, Xiaoan
Pereda-Lopez, Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Search completed: April 3, 2002, 05:46:33 Job time: 33753 sec

Perfect score: Scoring table:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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BG809582 mgct001xa
AL572700 AL572700
BBC34822 ML04H02 M
BF23465 HVSMEf000
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SP_1038_B
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1 (bases 1 to 1197)

2 Aslegbu.F.C. Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with Unpublished (2001)

Contact: Fred O. Aslegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:169015"
/clone="hasp001xa01f"
/clone_lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDNA library (hasp)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hasp001xa01f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Heterobasidion annosum/Pinus sylvestris mixed EST library cDNA clone hasp001xa01f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
3S
Location/Qualifiers
li .19 19
/organism="Heterobasidion annosum/Pinus sylvestris mixe
EST library"

'Ah xref="taxon:169015"
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AQ782679
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DEFINITION
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TITLE
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COMMENT
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                                                                         April 2, 2002, 18:47:35 ; Search time 3835.7 Seconds
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                                                                                                                                                                                                                                             22703874
    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                              11351937 seqs, 5372889281 residues
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                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                summaries
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Score

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105.2 104.6 100.4 99.2 98.4 98.9 97.2 96.6 95.8 95.8

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for
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/dev_stage="Seedling roots of scots pine were infected 6 days with H. annosum."

//note="Vector: pT-Adv: Sit_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)."

85 others
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Pred. No. 3.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750
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Unpublished (2001)
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Pred. No. 4.1e-09;
0; Mismatches 652;
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Tel: 466 18 67 15 50
Fax: +466 18 30 92 45
Email: Fred.Asiegbuenykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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/db xref+"taxon:169015"
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Stage Subtraction cDNA library (hasp)"

/dev_stage="Seedling roots of scots pine were infected for 6 days with H. annosum"

/note="Yector: pi-Adv; Site_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Helterobasian (FPS)."

##CLEODER AND STATE OF THE CONSTRUCTED FOR SCOTS PINE ROOTS OF STATE O
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B1416650 1015 bp mRNA EST 15-AUG-2001 hesp001xm01f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Heterobasidion annosum/Pinus sylvestris mixed EST library cDNA clone hasp001xm01f, mRNA
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Email: Fred Asiegbu@mykopat.slu.se
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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Seq primer: AATTAACCCTCACTAAAGGG
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hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycella of
ptherobasidon annosum (FP5)." 59 others
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1 (bases 1 to 1224)

Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.

Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.

Expressed sequence tags of randomly selected cDNA clones from the seedling roots of Scots pine (Pinus sylvestris)

Compublished (2001)

Contact: Fred O. Asiegbu

Dept. of Forest Mycology & Pathology

Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,

    1. .1224
/organism="Heterobasidion annosum/Pinus sylvestris mixed
EST library"

                                                                                                B1416537 1224 bp mRNA EST 15-AUG-2001 hasp001xe15f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Heterobasidion annosum/Pinus sylvestris mixed EST library cDNA clone hasp001xe15f, mRNA
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151 CCCCCCCCCCCCCCCCCCCCCCCCCCCCTTNCC 115
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
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Location/Qualifiers
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stage subtraction cDNA library (hasp)"
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hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycella of
Heterobasidon annosum (FP5)." 16 others
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Pred. No. 5.8e-08;
0; Mismatches 461; Indels
  Scots pine (Pinus sylvestris)
seedling roots of Scots pine (Pinus syl
Unpublished (2001)
Contact: Fred O. Asiegbu
Debt. of Forest Mycology & Pathology
Swedish University of Agriculture, Box
                                                                                 Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
                                                                                                                                                                                               /db_xref="taxon:169015"
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ilarity 44.2%;
Conservative
                                                                                                                                                                                  EST library"
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Matches 365; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              HVSMEF0020024f Hordeum vulgare seedling root EST 23-FEB-2001 (etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0020024f, mRNA sequence.
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Triticeae; Hordeum.
1 (bases 1 Lo 1159)
Wing R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development of a genetically and physically anchored EST resource
                                                                     1201 accgagctgaccctggcctgcggccccgacaaccgactcgccgaaaaaggctggaccacc 1260
                                                                                                                                                               cacaacaacacccacgqccacaccgaatggclaccaccaccccactcgaccacggccaa 1320
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Length 1159;
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                                                                                                                                                                                                                                                                                           Score 97.2; DB 11;
Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence stop: 1133
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Seq primer: AAFFAACCCTCACTAAAAGG
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/JLNL at:

Mww-blo.llnl.gov/bbrp/jmaqe.html

Linsert Length: 621 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 3']; double-stranded CDNA was ligated to Eco KI adaptors (Pharmacia), digested with Not I and cloned into Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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National Cancer Institute / National Institute of Neurold
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 289;
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .289
/organism="Homo sapiens"
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stage subtraction cDNA library (hasp)"

for stage="Seedling roots of scots pine were infected for 6 days with H. annosum"

/note="Weetor: pT-Adv; Site_1: BCORI; The subtractive hybridization cDNA library was constructed from scots hibrary was constructed from scots Heterobasidon (PP5)."

118 others
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/clone_lib="Heterobasidion annosum - Scots pine infection
                                                                                                 Asiagbu.F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                                       Unpublished (2001)
Conteact: Fred O. Aslegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
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Heterobasidion annosum/Pinus sylvestris mixed EST library
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Pred. No. 1.4e-07;
0; Mismatches 386; Indels 0
                                                                                                                                                                                                                                                                                          Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seg primer: T7 primer.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1. (bases 1 to 1348)
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253 ccaagcccgacgcccggccggcatcgccgacgccgatctcggacctcgtcgagcac; 312
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 1016)

1 (bases 1 to 1016)

Soest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Unpublished
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/db_xref-"taxon:99883"
/clone="036F09"
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Harity 45.2%; Pred. No. 1.6c-07;
Conservative 0; Mismatches 519;
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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source 1825 /organia /db_xref /clone====================================	Query Match Best Local Similarity 44. Matches 327. Conservative QY 645 ececeaangegquecaec QY 705 caaccccqueqqueacec QY 705 caaccccqueqqueacecc QY 705 caaccccqueqqueacecc QY 705 caaccccqueqqqqqqqqqqqqqqqqqqqqqqqqqqqqqq	674 825 614 885 554 945 494	Db
agitggctacctgacccccaagcgcgggccacctttgaagccgtgctagccaaactggc 689 CCGCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		gtateacacaaaegectagecteceggeceageggateatgetgttegecaaegacg 1109	BG786255 825 bp mRNA EST 20 MAY-2001 SEAUMC006212 Sea urchin primary mesenchyme cull chnA library Strongylocentrotus purpuratus chNA clone PC_0028_A2_A0B MK 5', mRNA sequence. BG786255 GI:14157268 EST Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Strongylocentrotus purpuratus Strongylocentrotus purpuratus Strongylocentrotus purpuratus Strongylocentrotus purpuratus Strongylocentrotidae; Echinodermate; Eleutherozoa; Echinozoa; Strongylocentrotidae; Echinodemate; Eleutherozoa; Echinoida; Strongylocentrotidae; Ethonogenes: Entinoida; Strongylocentrotidae; Strongylocentrotidae Strongylocentrotidae; Strongylocentrotidae Strongylocentrotidae; Strongylocentrotidae
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id_type-"embryo"
Lype-"primary mesenchyme cells"
rost-"E.coli ".coli; Site_1: Not1; Site_2: Sall; oligo
iming from poly A+ RNA, directionally cloned"
0 c 667 g 117 t 34 others
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nism="Strongylocentrotus purpuratus"
ref="taxon:7668"
=="PC_0028_A2_A08_MR"
-_1lb="Sea urchin primary mesenchyme cell cDNA
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4.1%; Pred. No. 1.7e-07;
Vc. 0; Mismatches 415; Indels 0;
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us-09-785-904-1.rst

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AQ748706.1 GI:5535952
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
              10-NOV-1999
Sperm Library D Homo
DNA sequence.
                                                                                                                                                                                                                                                                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib-"CIT Approved Human Genomic Sperm Library D" /sex="male"
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                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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            AQ895329 918 bp DNA GSS
HS_4832_A2_H01_T7A CIT Approved Human Genomic
sapiens genomic clone Plate=4832 Col=2 Row=O,
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Location/Qualifiers
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                                                                                                                   human.
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1 (bases 1 to 966)
Mahairas,G.C., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euleleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1004 ggaggtaccccaggcgatcttcgaccacggcacacccctggcgctgtatcacaccaaac 1063
                                                                                                                                                                                                 1124 coggetgigacgeaccegactaccacageccaageccacraegicacegectggaccagea 1183
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HS_5540_A2_AO3_SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1116 Col=6 Row=A, DNA sequence.
                                           .064 gcctagcctccccggcccagcggatcatgctgttcgccaacgaccgcggctgcaccaaac
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99780<sup>5</sup>819
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/db_xxef="texon:9606"
/clone="Plate=1116 Col=6 Row=A"
/clone_lib="RPCI-11 Human Male BAC Library"
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Location/Qualifiers
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BG809582
BG809582. GI:14180562
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

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                                                                                                     Score 95; DB 13;
Pred. No. 2e-07;
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                                                                                                                 Best_Local Similarity 41.4%;
Matches 293; Conservative
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/note="vector: pBlueScript SK(+) Vector; Site_1: EcoRI; Site_2: Xho1; The appressorium formation-specific CDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."
                                                                                                                                                                                                                                                                                                                                                                                                  /clone="mgct001xa24f"
/clone_llb="Magnaporthe grisea Appressorium Stage cDNA"
/dev_stage="Germinated conidia on apprressorium-inductive
surface"
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                                                                                                                                         Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Fax: 919-513-0024
Email: ralph_dean@ucsu.edn
Seg primer: T3 primer (AATTTAACCCTCACTAAAGGG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 94.4; DB 11;
45.4%; Pred. No. 2.5e-07;
Live 0; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                       /organism-"Magnaporthe grisea"
                                                                                                                                                                                                                                                                                                                                                      /strain~"70-15"
/db_xref~"taxon:148305"
                                                           Construction and sequence
library in the rice blast
Unpublished (2001)
Contact: Ralph A. Dean
  Sordariomycetes inceri
1 (bases 1 to 782)
Choi, W. and Dean, R.A.
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Best Local Similarity 45.4'
Matches 317; Conservative
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Search completed: April 2, 2002, 21:47:49 Job time: 10814 sec

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47.2 10. 45.6 10. 45.6 10. 45.6 10. 45.6 10. 45.6 10. 45.6 10. 45.6 10. 45.7 10. 45.9 9. 43.2 99. 43.2 99. 43.2 99. 43.2 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.7 10.0 90. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.6 99. 42.7 10.0 90. 42.6 99. 42.6 99. 42.7 10.0 90. 42.6 99. 42.7 10.0 90. 42.8 99. 42.9 90. 42.1 10.0 10.0 10.0 10.0 10.0 10.0 10.0 1	726-A. 7-1995. 7-1994; 9. 7-1993; 9. 7-1993; 9. 1 CORNELL 1 1 LW: 995-115442,
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	FT XX PN W09506 XX PF 09-MAP XX CORR XX PA (CORR XX PI Riley XX XX CORR XX CORR XX XX PA (CORR XX XX XX PA (CORR XX XX XX XX XX YX YX YX YX YX
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General, us; ic search, us; ic search, us; sill 2, 2002, sill 2, 2002, sill 2, 2004-3 sill 2, 20	Amatch Length DB ID 90.2 1535 16 AAQ89200 90.2 1535 17 AAT33656 90.2 1535 17 AAT33656 90.2 1535 19 AAV18647 77.5 650 19 AAV18649 77.5 650 19 AAV18649 12.3 12381 21 AAZ8381 12.3 12381 21 AAZ8381 12.3 12381 21 AAZ8381 12.3 12381 21 AAZ8381 11.6 3198 20 AAX02974 10.9 77536 21 AAA14651
Cog OM nucleic - nucleic Run on: Apri Title: US-C Perfect score: 453 Sequence: 1 ga Scoring table: IDEN Scoring table: IDEN Scoring table: IDEN Gapc Searched: 9306 Total number of hits Minimum DB seq length Maximum DB seq length A: 1: 1: 1: 1: 1: 1: 1: 1: 1: 1:	Result Score Ma Out No. Score Ma 2 408.4 9 9 4 4 4 4 9 9 1 7 7 7 2 1 7 7 5 7 2 1 1 6 8 55.6 11 9 55.6 11 6 52.4 1 1 6 9 4 1 10 52.4 1 10

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                                                                                                                                                                                                                                                                          The isolated DNA molecule of the invention confers on M. tuberculosis an ability to enter cells and to survive within macrophages. It encodes a polypeptide having a mol. wt. of about 50-55 kDa, pref. 52 kDa. The AA sequence represents a highly hydrophilic protein with a hydrophobic region at its carboxy terminus. It could be a secreted protein, a cytoplasmic protein, or a surface protein with its carboxy terminus attached to the outer membrane of the organism. The deduced AA sequence is in AAK71931.
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                                                                                                                                                                                          DB 16; Length 1535;
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DNA encoding for cellular uptake of Mycobacterium tuberculosis used to develop prods for vaccines, passive immunisation and diagnosis and cellular uptake of other materials
                                                                                                                                                                                           90.2%; Score 408.4; DB 16; Length
97.8%; Pred. No. 1.1e-78;
Live 0; Mismatches 6; Indels
                                                                                                                                                          Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M. tuberculosis cellular uptake gene region.
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181..810
                                              Claim 2; Page 9-11; 46pp; English.
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1126 gigciagicaaactggccgccccggcgcgaccaacccgacgacacaccccggicair 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 accteaecyacaccyaacycgeregeaacge-geateaecetgageaaceageaatacy 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A DNA molecule (AAT)3656) confers on Mycobacterium tuberculosis an ability to enter mammalian cells and to survive within macrophaues. The encoded protein sequence is given in AAM02301. The DNA was obtd. by ligating A. tuberculosis genomic DNA fragments into pBluescript invasive clones. The DNA includes 2 separate coding regions (Ser also AAT33657-58) coding for the cell entry (AAM02302) and macrophage survival (AAM02303) proteins. It can be used to produce the cellular uptake proteins used as vaccings or to facilitate uptake of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 gigctagccaaactggccgccccggcgcgaccaaccccgacgaccacaccccggtcatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA giving M. Luberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to protect mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 gtcccqaruagctgucccqctarqccaycgggtcatggactggctacaccccgarggq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 408.4; DB 17; Length 1545; Pred. No. 1.1e-78; ); Mismatches 6; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                     /product= macrophage survival protein
                    entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       materials, e.q. therapeutic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 41; 67pp; English.
                  /product= cell
886..1535
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                                                                /*tag= b
/label= ORF-2
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Best Local Similarity 97.8%;
Matches 446; Conservative (
/label= ORF-1
                                                                                                                                                                                                                                       96WU-US02155
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1406..10673
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                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium bovis strain BCG
                                                                                                                                                                                                                                                           AAT33537 standard; DNA; 12412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US01938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PATH-) PATHOGENESIS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stover CK;
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                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacqgcg 178
                                                                                                                                                                                                                                                                                                                                                                                                                          to enhance uptake of in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a Mycobacterium tuberculosis cellular uptake protein fragment, which confers on M. tuberculosis an ability to enter mammalian cells and to survive within mariophayes. The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g. antibiotics, DMA fragments or anti-incoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to treat unammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggatgtgtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 408.4; DB 19; Length 1535;
Pred. No. 1.1e-78;
); Mismatches 6; Indels 4;
                                                                                                                                                  DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1535 BP; 297 A; 544 C; 458 G; 236 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis DNA - confers ability therapeutic agents e.g. antiblotics, also useful
                                                                                                                                                                     Cellular uptake protein; vaccine; infection; ds.
                          cacgaegggetgetggeegggetgegegetgate 453
                                                                                                                                                                                                                                          /note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Pages 9-10; 82pp; English.
                                                                                                                                                                                                             Location/Qualifiers
1..1534
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ilarity 97.8%;
Conservative (
                                                                                         AAV18647 standard; DNA; 1535
                                                                                                                                                                                                                                                                                                                         96US-06894<u>11</u>.
                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                (first entry)
                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-145620/13.
P-PSDB; M:W47541.
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Matches 446; Conserv
                                                                                                                                                                                                                                                                                                                                                                             Riley LW;
                                                                                                                                                                                                                                                                                                        06-AUG-1997;
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                                                                                                                                03-JUL-1998
                                                                                                                                                                                                                                                                                     12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                            Chong P,
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This DNA sequence comprises Mycobacterium bovis BCG deletion sequence BCGdelta3. A specific genetic deletion of this region results in an avirulence phenotype of the mycobacterium. 2 Other deletion regions (see AAT131535 and AAT131316) have also been detected. Identification involved screening a BCG cosmid library with a radiolabeled probe obtained following DNA subtraction between virulent Mycobacterium tuberculosis H13Rv and avirulent BCG. The deletions provide useful markers for the identification of an avirulent, or a virulent, mycobacterial phenotype. Determination of avirulence requires the detection of the presence or absence of
                                                                                                                                                                                                                                         gigotagocaaactygocyccoccyggogogogaccaaccocgaccacaccoccygtcaic 357
                                                                                                                      acggcatglcacqgctaagtggctacctgacccccaagtcgcgggccacctttgaagcc 297
                                                                                                                                                                                                                                                                             gacaccarrecenditycynecyneatrgaccqcgacaccgcagccaagcccaaryraac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCG delta 3; virulence; avirulence; attenuation; gene deletion; mycobacteria; vaccine; infection; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to coacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*ray= a
/wore= "BCG delta l deletion region"
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                                                                                                                                                                                  cgacgagetggecegetacgeceagegggteatggaetggetacaeeecegaeggegaeet 182
                                                                                                                                                                                          361
                                                                                                                       522 tgtccaaacccgccaggccgccgaagcccgacctggccgcaaaccgctcaaatatcgtcc 581
                                                                                                                                                                                                                           aggogcacatcaaagtgattcgcgccctttttcgccc-acctgcccgccgcggtggatg 66
the deletion; the deletions are detected either by detecting the presence or absense of deletion junctions (see AAT3538-46), or by detectin the presence or absence of the sequences contained within the deletion. Deletion polypeptides are used as components of immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                     caccgacaccgaacgcgcccgcaaacgc-gcatcaccctgagcaaccagcaatacgacgg
                                                                                                                                                                                                                                                                                                                        ccaccccgatgcggccgccatcgaccgcgaccgcgcagccaagcccaacgcaaccacg
                                                                              Length 12412;
                                                                                                8;
                                                   Sequence 12412 BP; 2146 A; 4273 C; 3876 G; 1917 T; 200 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell entry; macrophage survival; vaccine;
                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis strain H37Ra (ATCC 25177)
                                                                            Score 366.8; DB 17;
Pred. No. 9.1e-70;
); Mismatches 12; I
                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        acgggctgctggccgggctgcgcgctgatc 453
                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis macrophage survival gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               passive immunisation; gene therapy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                           81.0%;
llarity 95.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                            Query Match
Best Local Similarity
Matches 432; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   AAT33658 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9626275-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT33658;
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A DNA molecule (AAT3365B) codes for a protein (AAW02303) that confers on Mycobacterium tuberculosis an ability to survive within macrophages. It is a fragment of a larger molecule (AAT33656) obtd. by ligating M. tuberculosis genomic DNA fragments into pBluescript I vector and screening recombinant E. coli strains for Hela cellinvasive clones. It can be incorporated into a vector and used for prodn. Of recombinant macrophage survival protein, which is useful in vaccines or for facilitating uptake of other materials, e.g. therapeutic genes, into mammalian cells. A second DNA molecule tuberculosis the ability to enter mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 cgtcccqacgaqctqqcccqctacgccagcgggtcatggactggctacaccccqacggc 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 cgtcccgacgagottggcccgctacgcccagcgggtcatggactggctacaccccgacggc 120
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                                                                                        vaccines to protect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 cyanacharnningatynyynynnynatriyanggganaccogcagccaagccaangcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.5%; Score 351; DB 17; Length 650; larity 97.7%; Pred. No. 1.9e-66; Conservative 0; Mismatches 5; Indels
                                                        DNA giving M. tuberculosis ability to enter mammalian cells and/or survive within macrophage(s), useful in vaccines to p mammals against Mycobacterium tuberculosis infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA for M. tuberculosis cellular uptake protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 ccaeqaeqqeeqqeeqqqeeqqeeqeetgale 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cellular uptake protein; vaccine; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                            Claim 7; Page 45; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР
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WPI; 1996-425086/42.
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Matches 388; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                       P-PSDB; AAW02303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            egtecegaegagetggeeegetaegeeeagegggteatggaetggetaeaeeeegaegge 120
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                60 gtggatgtgtccacccgccaggccgccgaagccgacctgccygcaaaggc--ctcaatat 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gtggatgtgtccacccgccaggccgccgaagccgacctggccggcaaagccgctcaatat 60
                                                                                                                                                                                              Mycobacterium tuberculosis DNA ^\circ confers ability to enhance uptake therapeutic agents e.g. antibiotics, also useful in vaccines
                                                                                                                                                                                                                                                The present sequence encodes a Mycobacterium tuberculosis cullular uptake protein fragment, which confers on M. tuberculosis an ablility to survive within macrophages.

The protein can be used in a vaccine to prevent M. tuberculosis infection, and provide for the uptake in cells of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotics, DNA fragments or anti-neoplastic agents. Antibodies raised against it can be used to treat mammals already exposed to M. tuberculosis, to induce a passive immunity and prevent disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtgctagccaaactggccgccccggcgcgcaccaaccccgacgaccacaccccggtcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 egigetagecaaaciggeegeeeceggegegaecaaceeegaegaecacaeeeeeggicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgacaccaccccgatgcggccgccatcgaccgcgacaccccgcagccaaqccaacgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgacaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 650;
                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                        Sequence 650 BP; 123 A; 258 C; 185 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                     77.5%; Score 351; DB 19; 97.7%; Pred. No. 1.9e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 ccacgacgggctgctggccgggctgcgcgctgatc 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "stop codon not given"
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                              Disclosure; Page 14; 82pp; English.
                                                                                                                         (CORR ) CORNELL RES FOUND INC
                                                                     97WO-US13056
                                                                                          96US-0689411
                                                                                                                (CONN-) CONNAUGHT LAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                           Matches 388; Conservative
                                                                                                                                                                 WPI; 1998-145620/13.
                                                                                                                                            Chong P, Riley LW;
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                            P-PSDB; AAW47543
                              W09805784-A1
                                                                       36-AUG-1997;
                                                                                           07-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA: (2) expression vectors containing the DNA: (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformed; (5) preparation of avermectin aglycon or its derivatives by culture of transformed avermectin producing microor-quisms; and (6) oligomerterlides of 5-60 bases in length containing sense on antiscuss sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avermectin adjycone synthase DNA and proteins encoded by all or part of it for the production of avermectin and its derivatives for drug and agrochemical use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22011 caccacctcatcacccaacgcgccacctcatgcaaaccatgcccccggcaccatgac 22070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21951 acactecetegggaaateaeegeegeegeetegeeggeateeteaeegaege 22010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 aaccancaatacgacggcatgtcacggctaagtggctacctgacccccaagtcgcyggc 284
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use as drugs, veterinary drugs and agrochemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acacccegacygogacctcaccgacacygacgcccgcaaacgcgcatcaccctgage 224
                                                                                                                                  Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis; multifunctional enzyme; polyketide; avermectin; veterinary drug;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents DNA which encodes avermectin aglycon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cacctttgaagccgtgctagccaaactggccgccccggcgacgaccaaccccgacgacca
                                                                 S. avermitilis avermectin aglycon synthase DNA aveAI SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                  /*tay- a
/note= "avermectin aglycon synthase protein"
11971..30690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "avermectin aglycon synthase protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Best Local Similarity 52.5%; Pred. No. 0.00083;
Matches 125; Conservative 0; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 66-134; 314pp; Japanese.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-JP01041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-565458/52.
P-PSDB; AAB23749, AAB23750.
(first entry)
                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KITA ) KITASATO INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda H;
                                                                                                                                                                                                       agrochemical; ds.
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10-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Omura S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285
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AAA92301 standard; DNA; 30690 BP

AAA92301 ID AAA9

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Best Local S
Matches 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           host cells, and methods for producing novel polyketides by culturing host cells are claimed. The polyketides obtained are useful as antibiotics and insecticides. Fermentation products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with reduction. Novel PKS are provided in which in which the reductive loop in a selected module of the Type I PKS is replaced with the equivalent segment from the same or different PKS gene cluster or by a mutated or synthetic segment. Vocious and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of DNA encoding the first 2 modules of the avermectin polyketide synthase (PKS) of Streptomyces avermitilis. The invention relates to nucleic acids encoding a Type I PKS such as avermectin in which a polylinker with multiple restriction sites replaces or 1 more PKS genes encoding enzymes associated with reduction. Novel PKS are provided in which in the control of the provided in which in the control of the pks are provided in which in the control of the pks are provided in which in the control of the pks are provided in which in the pks are pks a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutated Type I polyketide synthase containing a extension module for replacement of a reductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12381 BP; 1884 A; 4561 C; 4005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing C22-C23 dihydroavermectin, ivermectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7a-f; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing polyketides, e.g. Bl avermectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-182117/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                       165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200001827-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis avermectin polyketide synthase modules 1+2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-2000
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                                                   285
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cacctttgaagccgtgctagccaaactggccgccccggcggcgaccaaccccgacgacca
                                                                                                                                                                                                                                                                                                                                        acaccccgacggcgacctcaccgacaccgaacgcgcccgcaaacgcgcatcaccctgagc 224
                                                                                                                        caccaccctcatcacccaacgcgccaccctcatgcaaaccatgccccccggcaccatgac
                                                                                                                                                                                                          aaccagcaatacgacggcatgtcacggctaagtggctacctgacccccaagtcgcgggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
124; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOTICA TECHNOLOGY LTD. PFIZER INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55.6; DB 21; Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 1931 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polylinker site loop sequence, f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 12381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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20

Matches 124; Query Match Best Local :

Conservative

0;

Pred. No. 0.0018; 0; Mismatches 114; Score 55.6; DB: Pred. No. 0.0018

Indels

Gaps

0;

DB 21;

31422; 0;

Local Similarity

12.3%;

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                                            or its derivatives by culture of transformed avermectin-producing microorganisms; and (6) oligonucleotides of 5-60 bases in length containing sense or antisense sequences from the avermectin aglycon synthase DNA. The enzymes are useful for the production of modified forms of avermectin and of the intermediates in its biosynthesis, for
                                                                                                                       synthase proteins. Also described are: (1) polypeptides encoded by all or part of the DNA; (2) expression vectors containing the DNA; (3) host cells transformed by the vectors; (4) preparation of the polypeptides by culture of the transformants; (5) preparation of avermectin aglycon
Sequence 31422 BP; 4136 A; 10238 C; 11677 G; 5371 T; 0 other;
                             use as drugs, veterinary drugs and agrochemicals.
                                                                                                                                                                                        The present sequence represents DNA which encodes avermectin aglycon
                                                                                                                                                                                                                  Claim 2; Page 134 203; 314pp; Japanese.
                                                                                                                                                                                                                                                      agrachemical use
                                                                                                                                                                                                                                                                   Avermectin aglycone synthase DNA and proteins encoded by all or part it for the production of avermectin and its derivatives for drug and
                                                                                                                                                                                                                                                                                                                P-PSDB; AAB23751, AAB23752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agrochemical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis; avermectin aglycon synthase; biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. avermitilis avermectin aglycon synthase DNA aveAII
                                                                                                                                                                                                                                                                                                                                                                                             (KITA ) KITASATO INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-2000; 2000WO-JP01041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 - AUG - 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multifunctional
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                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0046961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enzyme; polyketide; avermectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "avermectin aglycon synthase protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "avermectin aglycon synthase protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14824..31422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Query Match
Best Local Similarity
Matches 182; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibition; interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthritis; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; growth factors; treatment; IL-1 receptor complex; BAC; ss.
                                                                                                    Tango-77 is a member of the cytokine superfamily that is expected to inhibit inflammation by binding to the interleukin-1 receptor (IL-1R). I may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines and growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-1998;
04-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IL-1ra BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX02974 standard; DNA; 3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09906426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                         AXX02956-X03048 and AXX22301-X22304 are overlapping BAC genomic sequences containing alternatively spliced forms of human IL-Ira. Such fragments are used in the method of the invention which describes the isolation of a novel human TANGO-77 encoding nucleic acid and protein.
                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators
                                                                                                                                                                                                                                                                                                                                                                                                                             Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345
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                                                                         Sequence
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                                                                            3198
                                                                                                                                                                                                                                                                                                                      Figure 3;
   Conservative
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                                                                            BP;
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97US-0054646.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contiguous DNA sequence
                                                                            807 A;
                11.6%;
45.6%;
                                                                            847 C;
                                                                                                                                                                                                                                                                                                                        English
 Score 52.4; DB 2v,
Pred. No. 0.008;
""" atches 217;
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                                                                              681 G;
                                                                              846 T; 17
                                                                                other;
        Indels
                                 Length
                                      3198;
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AAA14651/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune chronic active hepatitis; inflammatory bowel disease; multiple sclerosis; primary biliary cirrhosis; scleroderma; neurite outgrowth; nerve regrowth; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant; streptomyces hygroscopicus var. ascomyceticus; immunophilin; FK-506 binding protein; polyketide compound; transplant rejection; graft-versus-host disease; uveitis; alopecia universalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3153
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                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral neuropathy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the FK-520 biosynthetic
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                                                /note= "fkbF
8156..8824
                                                                                                                                                                                                                                                                     /note= "fkbR2 gene"
complement (4595..5488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (412..1836)
/*tag= g
/note= "fkbG
                                                                                                                         6808..8052
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                                                                                                                                                                                                                                                                                                                                                                   /noté= "fkbV gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "fkbW gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*1 ag=
                                                                                                   /*tag=
                                                                                                                                              /note= "fkbE gene"
                                                                                                                                                                                                                       /noté- "fkbRl gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stroke; traumatic spinal cord; brain injury;
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  gene"
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E.L.																																	
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<pre>/note= "KR3" complement (2986931018)</pre>		/note= "ACP3" complement (2909229740)		₹.	4	₹.	complement (2614627430) /*tag= ab	<pre>/*tag= aa /note= "DH4 (inactive)"</pre>	<pre>/note= "ACP4" complement (2499726146)</pre>	complement (2416324373) /*tag= z	/*tag= y /note= "fkbB gene"	complement (2399246573)	3 ,	/note= "AT5" complement (2265323892)	complement (2142022653) /*tag= w		∄ .	complement (1946420097) /*tag= u	Complement (1911019320) /*tag= t /note= "ACP5"	/*tag= s /note= "KS6"	/noteracy transferase domain (AT) 6" complement (1782019053)	ne .	me ,	/note= "KM6" complement (1451715294) /*tag= p		06"	/^Lag= m /note= "fkbC gene" complement (1345213662)	ne .	/note= "fkbK gene" complement (1211313150) /*tag= 1	nent k	ment j	oI gene"	<pre>/*tag= h /note= "fkbH gene" complement (989410994)</pre>
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Best Local Similarity
Matches 134 · Conserv
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Pred. No. 0.04;
0; Mismatches 141;
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Best Local Similarity
Matches 154; Conserv
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                                                                                                                                                                                                                     Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor positive breast cancer; therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA02484 standard; cDNA; 1000
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                                                                                                                                                                                             oestrogen receptor-negative breast cancer; lung cancer; ss
                                                                                                                                                                                                                                                                                                                                       Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475
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P-PSDB; AAR22197.
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and free of protease

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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1000 BP; 21 A; 53 C; 574 G; 22 T; 330 other;
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(HYSE-) HYSEQ ]
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                                                                                                                                                                                                                                                                                                  agccgacctgccggcaaaggcctcaalatcglcccgacgagclggcccgclacgccagc 148
                                                                                                                                                                                                                                                                                                                                   cgcgccctttttcgcccacctgcccgccgcggtggatgtgtccacccgccaggccggca
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gcgacacccgcagccaagcccaacgcaaccacgacgggctgctggccgggctgc 442
                                                          ccaaccccgacgaccacaccccggtcatcgacaccaccccgatgcggccgccatcgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 994; 1097pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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98US-0085537.
98US-0085696.
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98US-0105877
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Garcia V, Jon
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Randazzo F, I
                                                                                                                                                                                                                                                                                                                                                                                              Score 47.2; DE Pred. No. 0.097 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               0;
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ຊື່ 272;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 1000;
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AAZ17038/c
ID AAZ170
cc of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The cc polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, and detection of polynucleotides con be used for a variety of purpose, e.g. detection of expression levels, can be used for raising antibodies for experimental, diagnostic and cc detection of polynucleotides polynucleotides can be used for raising antibodies for experimental, diagnostic and cc detect of diagnostic and cc detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to condition of such that it is polynucleotides of the invention are especially used in the cc and lung cancer. The polynucleotides of the invention are especially used in the candidate analogues and antagonists.
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24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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Lamson G, Leshkowitz D, Pot D, Randazzo F, Re
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic analysis; colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene expression product cDNA sequence SEQ ID NO:4508.
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                                                                                                                                                                                                                                                                                                                                                differentially expressed dene product in a test sample from a cell
                                                                                                                                                                                                                                                                                                                                                                a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a library of human polynucleotides comprising the sequences given in AAX12532 to AAX17779. Also described is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 2137; 2479pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human genes and their expression differentially expressed in different c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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980S-0075954.
980S-0080114.
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                                      and antagonists.
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Search completed: April 2, 2002, 22:49:09 Job time: 9209 sec
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                                                                                  tggcccgctacgcccagcgggtcatggactggctacaccccgacggcgacctcaccgaca 190
                                         caccegecaggeegeegaageegacetgeeggeaaaggeeteaatategteeegaegage 130
                       Gaps
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                                                                                                                                        251 getaagtggetacetgacceccaagtcgcgggccacetttgaagccgtgctagccaaac
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Length 1454;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human gene expression product cDNA sequence SEQ ID NO:4735.
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Score 47.2; DB 20; Length
Pred. No. 0.099;
0; Mismatches 225; Indels
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
Jones ML, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                    1060 CCCNCACNGCGCCGCACNC 1042
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98US-0072910.
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                       Conservative
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            Similarity
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03-APR-1998
                        153;
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ1253 to AAZ1779. Also described is method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polynuclpolisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two calls (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 aagtegegggeent tigaageegigeeaageeaaaetggeegeeeegggggeegae 333
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; Mismatches 296;
differentially expressed in different cell types
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                                                                          Claim 1; Page 2250-2251; 2479pp; English.
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29.5%;
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Matches 124; Conservative
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Sequence 1, Appl. Sequence 1, Appl. Sequence 3, Appl. Sequence 38, Appl. Sequence 4, Appl. Sequence 6, Appl. Sequence 7, Appl. Sequence 7, Appl. Sequence 7, Appl. Sequence 1, Appl. Sequence 1, Appl. Sequence 3, Appl. Sequence 1, Appl. Sequence 1,

Sequence 1, Sequence 1, Sequence 1,

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GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Uses thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,727
REFERENCE/DAYKET NUMBER: 19603/185 (D-1485B)
TELECOMMUNICATION INFORMATION:
US-09-320-878-22
US-07-705-490-1
US-08-455-073A-1
US-08-455-073A-1
US-09-105-537-3
US-08-818-112-138
US-08-918-662-4
US-08-918-662-4
US-09-430-854-7
US-09-312-034A-1
US-09-312-038-3
US-09-312-038-3
US-09-312-038-3
US-09-312-038-3
US-09-312-038-3
US-09-312-038-3
US-09-312-038-3
US-08-87-427-1
US-08-87-427-1
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Pred. No. 3.3e-80;
0; Mismatches 6
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                                                                                                                                                                                                                                                               US-08-439-009A-1
                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 18M PC COMPATIBLE OPERATING SYSTEM: PC-DGS/MS-DGS
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; Patent No. 6008201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
US-08-464-052-1
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TELEPAX: (716) 263-1600
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
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97.8%;
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NAME: Goldman, Michael L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.2
Best Local Similarity 97.8
Matches 446; Conservative
                 double
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STATE: New York
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   STRANDEDNESS:
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ZIP: 14603
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Sequence 16, Appl
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                                                                                                         April 3, 2002, 05:46:33 ; Search time 165.4 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                 Compugen Ltd
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4 US-08-461-002-1
4 US-08-469-411-1
5 PCT-US94-09863-1
3 US-08-30-878-18
3 US-08-30-878-18
4 US-08-461-002-5
4 US-08-689-411-5
3 US-09-103-8408-2
4 US-09-103-8408-2
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US-08-458-745-1
US-08-46-814-4
US-08-286-304-6
US-08-442-745-6
US-08-442-745-6
US-08-443-129-6
US-08-443-130-6
US-08-898-911-6
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US-09-105-537-15
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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length: 2000000000
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453
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Match Length DB
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TITLE OF INVENTION: DNA MOLECULE FRAGMENTS ENCODING FOR TITLE OF INVENTION: CELLULAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES TITLE OF INVENTION: THEREOF CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/689,41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-689-411-1
Sequence 1, Application US/08689411
Patent No. 6224881
GENERAL INFORMATION:
APPLICANT: R1ley M.D., Lee W.
APPLICANT: Chong, Pele
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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LENGTH: 1535 base pairs
TYPE: nucleic acid
   Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rochester
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   Matches
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                                                                                     1186 GACACCACCCCGATGCGGCCGCATCGACCGCGCACCCCGCAGCCCAACGCAAC
                                                                                                                                                    gtcccgacgagctggcccgctacgcccagcggggtcatggactggctacaccccgacggcg 178
tggatgtgtccacccgccaggccgccgaagccgacctgccggcaaaggc--ctcaatatc 118
                                                                                                                                    aceteacegacacegaacgegecegeaaacge-geateaceetgageaacageaataeg
                                                                                                                                                                                                                                                                                                                                           gacaccecccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/186 (D-1485B)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 408.4; DB 4
Pred. No. 3.3e-80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/461,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08461002
; Patent No. 6214543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Riley M.D., Lee W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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97.8%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 14603
COMPUTER READABLE FORM:
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CLASSIFICATION: 435
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STATE: New York
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US-08-461-002-1
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Query Match
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                                                                                                                                                                                                                                                                                                                    179 acctcaccgacaccgaacgcgccagcaacgc-gcatcaccctgagcaaccagcaatacg 237
                                                                                                                                                                      827 GATCGCCGAGCCCCACGTCAAAGTGATTCGCCGCCTTTTTCGCCCCACCTGCCCGCCGG 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 gacaccaccccgatgcggccgccatcgaccgcgacacccgcagccaagcccaacgcaac 417
                                                                                                                                             1 gateggegagegeacateaaagtgattegegeetttttegeecacetgeeegegg 60
                                                                                                                    Gaps
                                                                                                                                                                                                                                                             gtcccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacgqcg
                                                                                                                   4;
                                                                                      Length 1535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RILEY, Lee W.
TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR
TITLE OF INVENTION: UPTAKE OF MYCOBACTERIUM TUBERCULOSIS
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09863
                                                                                                                . 9
                                                                                   Score 408.4; DB 4
Pred. No. 3.3e-80;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
MAME: Goldman Mr., Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/FOCKET NUMBER: 19603/180 (D-1485)
TELECOMMUNICATION INFORMATION:
TELECHONE: (716)263-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1246 CACGACGGCTGCTGGCCGGCTGCGCCGCCTGATC 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application PC/TUS9409863 GENERAL INFORMATION:
             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                   Query Match 90.2%;
Best Local Similarity 97.8%;
Matches 446; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-09863-1
                                          US-08-689-411-1
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358 gacaccaccoccarycantegaccocygacaccoccagccaaccaaccaacycaac 417 [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [1111] [111] [1111] [1111] [1111] [1111] [1111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [111] [11
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APPLICANT: WHITE, Owen R.
APPLICANT: WHATE, Usen R.
APPLICANT: WHATE, Owen R.
APPLICANT: VEN'ER, Claire M.
APPLICANT: VEN'ER, Claire M.
APPLICANT: VEN'ER, Claire M.
TITLE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007:00
CURRENT APPLICATION UNIMBER, US/09/103,840A
CURRENT FILLING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acqgcatqtcarqqctaaytqgctacctgaccccaagtcgcgggccacctttgaaqcc
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Pred. No. 3.3e-80;
0; Mismatches 6;
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: Patent No. 6294338
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%;
TELEFAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1535 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 1
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CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simil
Matches 446; C
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PCT-US94-09863-1
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Length 4411529;

4;

DB

Score 408.4;

90.28;

single

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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-464-052-5
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Db 1789400 TGGATGTCTCCACCCGCCAGGCCGCACCTGGCCGGCAAAGCCGCTAAAATC 1789341

    QY
    119 gtcccgacgactggcccgctacgcccaqcgggtcatggactggctacaccccgacggcg 178

    Db 1789340 GTCCCGACGACGACGCCCCCACCGGGGTCATGGACTGGCTACACCCCCACGGCG 1789281

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      QY
      298
      gtgctagccaaactggccgccccggcggcgaccaaccccgacgaccaccccggtcatc
      357

      Db
      1789161
      GTGTAGCCAAACTGGCCGCCCCGGGGCGAACCAACCCCGACAACACCCCGGTCATC
      1789102

                                                                                                  Db 1789460 GAICGCCGAGGCGCACGTCAAAGTGATTCGCGCCCTTTTTTCGCCCACCTGCCGCGGG 1789401
                                                                                                                                                                                                                                                                                                                                                             Db 1789280 ACCTCACCGACACGACGCCCCCAAACGCGCGATCACCCTGAGCAACCAGCAATACG 1789221
                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 1789220 ACGCCATGTCACGCCTAAGTGGCTACCTGACCCCCCAAG-CGCGGCCCCTTTGAAGCC 1789162
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                                                                                                                                                                                                                                                                                                                                  179 accteacegacacegaaegegecegeaaege-geateaceetgageaaceageaataeg 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 gacaccaccccgatgcggccgccatcgaccgcgacccgcagccaagccaacgcaac 417
                                                                                                                                                                                                                                                                                                                                                                                                                     238 acggcatgtcacggctaagtggctacctgacccccaagtcgcgggccacctttgaagcc 297
                                            Gaps
                                                                              1 gatcggcgaggcgcacatcaaagtgattcgcgcctttttcgcccacctgccgcggg 60
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APPLICANT: Mahairas, Gregory G.
TTLEOF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
TTLEOF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: To neo Market Plaza, Steuart Street Tower, 20th
STREET: California
CUTY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,878 FILING DATE: 17-FEB-1995 CLASSIFICATION: 435
           97.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08390878
Patent No. 5700683
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 1537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 12412 base pairs
nucleic acid
               Best Local Similarity 97.8
Matches 446; Conservative
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: DNA MOLECHIE Encoding for Cellular
TITLE OF INVENTION: Uptake of Myrobacterium Tuberculosis and Uses thereof
                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 caccgacaccgaacqcgcccgcaaacgc-gcatcaccctgagcaaccagcaatacqacgq
                                                                                                                                                                                                                                                                                                                302 tagccaaactggccgccccggcgcgaccaaccccgaccaccaccccggtcatcgaca
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                                                             Length 12412;
                                                                                        12; Indels
                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                            Score 366.8; DB Pred. No. 3.7e-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19603/185 (D-1485B)
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Nixon, Hargrave, hevans & STREET: Clinton Square, P.O. Box 1051 CIFY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08464052
Patent No. 6008201
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 1960
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1BM PC compatible
DNA (genomic)
                                                       Query Match
Best Local Similarity 95.6%;
Matches 432; Conservative
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MEDIUM TYPE: Floppy
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COUNTRY:
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                                                                                                                                                                                            Query Match
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APPLICANT: Riley M.D., Lee W.
TITLE OF INVENTION: DNA Molecule Encoding for Cellular
TITLE OF INVENTION: Uptake of Mycobacterium Tuberculosis and Usrs thereof
NUMBER OF SEQUENCES: Up
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                           9acctcaccgacaccgaacgcgcccgcaacgc-gcatcaccctgagcaaccagcaatac 236
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                                                                                                                                                            Length 650;
                                                                                                                                                                                       Indels
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                                                                                                                                                           77.5%; Score 351; DB 3; 97.7%; Pred. No. 7.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08461002 Patent No. 6214543
                                                LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-464-052-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
(716) 263-1304
        TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      Matches 388; Conservative
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                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                            Query Match
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DNA MALECULE FRAGMENTS ENCODING FOR CELLUIAR UPTAKE OF MYCOBACTERIUM TUBERCULOSIS AND USES THEREOF
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Pred. No. 7.2c-68;
); Mismatches 5; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doyle LLF
            19603/186 (D-1485B)
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5 Patent No. 6224861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                               ; 'TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-461-002-5
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97.78;
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                                                                                                                                                                                                                                              LENGTH: 650 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 388; Conservative
                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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OPERATING SYSTEM:
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U.S.A.
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CITY: Rochester
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Fatent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: 094-04/052001
CURRENT FILING DATE: 1998-08-03
EARLIER PLILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FALESEQ for Windows Version 3.0
SSOFTWARE: FALESEQ for Windows Version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                               60 gtggatgtgtccacccgccaggccgaagccgacctgccggcaaaggc--ctcaatat 117
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Pred. No. 7.2e-68;
O; Mismatches 5;
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/187
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         ; MOLECULE TYPE: DNA (genomic)
US-08-689-411-5
                                                                                    TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                   77.58;
97.78;
      ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael I
                                                                                                                                                  LENGTH: 650 base pairs
                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.7'
Matches 388; Conservative
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
CLASSIFICATION: 536
                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
FEATURE:
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    Db 1780338 GAYCGCCAGGCGCACATCAAAGTGATTCGCCCCTTTTTTCGCCCACCTGCCCGCGG 1780279

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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: UNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: UNERTHOUSIS
TITLE OF THE FREENCE: 24 465, 20007, 00
CURRENT APPLICATION NUMBER: US/OY/103, 840A
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                                                                                                                                                                                                                                                                                                        Length 152331;
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                                                                                                                                                                                                                                                                                         11.6%; Score 52.4; DB 3;
ilarity 45.6%; Pred. No. 0.003;
Conservative 0; Mismatches 217;
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Pred. No. 0.018;
0; Mismatches 5;
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NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or
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98.0%;
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ 1D NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 2
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Best Local Similarity 98.0
Matches 447; Conservative
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Best Local Similarity
Matches 182; Conserv
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3870029 acggtatgtcacggctaagtggctacctgacccccaag-cgcgggccacctltqaaqcc 3870087
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                                  1780278 TGGATGTGTCCACCGCCAGGCGCCGACCGACCTGGCCGCCAAAGCCGCTCAATATC 1780219
                                                                                          1780158 ACCTCACCGACACCGACACGCCCGCAAACGCGGCATCACCCTGAGCAACCAGCAATACG 1780099
                                                                                                                                                                                                                                                                             1780098 ACGCCATGTCACGGCTAAGTGGCTACCTGACCCCCCAAG-CGCGGGCCACCTTTGAAGCC 1780040
                                                                                                                                                                                                                                                                                                                                                         1780039 GTGCTAGCCAAACTGGCCGCCCCGGGGCGAACCCCGACCACCACACCCCGGTCATC 1779980
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                  tggatgtgtccaccgccaggccgccgaagccgacctgccggcaaaggc--ctcaatatc 118
                                                                                                                                                                          179 aceteaccgacaccgaacgcgcccgcaaacgc-gcateaccctyagcaaccaqcaatacg 237
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FASSER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN;
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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; OTHER INFORMATION: "n" bases at various
; OTHER INFORMATION: represent a, t, c or
US-09-103-840A-2
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Matches 443;
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APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalio
APPLICANT: Engel, Natalio
APPLICANT: Engel, Natalio
APPLICANT: Dispet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-20555/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT APPLICATION NUMBER: PCT/EP96/03643
EARLIER APPLICATION NUMBER: PCT/EP96/03643
SAFWARE: PAEDLING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 11
SOFWARE: PAEDLIN Ver. 2.0
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99;
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                                                                                                                                          Sequence 4, Application US/09029603 Patent No. 6210935
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nes 104; Conservative
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OTHER INFORMATION: ORF
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LOCATION: (1747)..(2553)
OTHER INFORMATION: ORF
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: LOCAFTON: (5071)..(6085)
: OTHER INFORMATION: ORF
US-09-029-603-4
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OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCATION: (4013)..(
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RESULT 15
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Db 3883955 tggatgtgtccacccgccaggccgccgaagccgacctgyccggcaaagccgctcaatatc 3884014

      QY
      179 acctcaccgacaccgaacgcccgcaaacgc-gcatcaccctgagcaaccagcaatacg 237

      Db
      3884075 acctcaccgacaccgaacgcgccgcaaacgcggcatcaccctgagcaaccagcaatacg 3884134

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                    5418 ggtcgaggcggtcaccgaacgcacccgctgcctgctcccggtccacctgtacggcca 5477
309 actggccgccccggcgaccaaccccgacgaccacaccccggtcatcgacaccaccc 368
                                                                                     238 acggcatgtcacggctaagtggctacctgacccccaagtcgcgggccacctttgaagcc 297
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Olaire M.
APPLICANT: VENTER, Olaire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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Pred. No. 0.32;
0; Mismatches 6; Indels 4;
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CTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                  5478 gtgcgtcgacatggcgccgctga 5500
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                         429 gctggccgggctgcgcgctga 451
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.6
Best Local Similarity 97.8
Matches 446; Conservative
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LENGTH: 4411529
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US-09-103-840A-1
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280 egggceacctttgaagccgtgctagccaaactggccgccccggcggcgaccaacccgac 339
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Pred. No. 0.17;
0; Mismatches 76;
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                                                                                                                                                                                                                                                                    FRAGILE X SYNDROME
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RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) R36-6600
                                                                                                                                                                            MULLEY, John C
MANDEL, Jean-Louis
PRITCHARD, Melanie April
LYNCH, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/638,518
FILING DATE: 04-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/802,650
FLING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
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FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200 FILLING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/672,232 FILING DATE: 20-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
Sequence 1, Application US/08118200
Patent No. 6197500
                                                                     RICHARDS, Robert I
SCHLESSINGER, David
                                                      SUTHERLAND, Grant R
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IBM PC compatible
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                                                                                                       NAGARAJA, Kamaiah
KREMER, Eric J
                                                                                                                                            YU, Sni
BAKEK, Elizabeth
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 53.9%;
Matches 89; Conservative
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COUNTRY: United States
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CORRESPONDENCE ADDRESS:
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EDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                             APPLICANT: LYNCH, M
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
                                 GENERAL INFORMATION:
APPLICANT: SUTHER
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Oy Db

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Search completed: April 3, 2002, 08:04:13 Job time: 42013 sec

Copyri	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic . nucleic search, using sw model	ırch, using sw model
Run on: April	April 2, 2002, 21:47:49; Search time 3835.7 Seconds (without alignments) 1269.087 Million cell updates/sec
Title: US-09-7 Perfect score: 453 Sequence: 1 gatcg	US-09-785-904-2 453 1 gatcggcgaggcgcacatcaccgggctgcgcgcgcgtgatc 453
Scoring table: IDENTITY_NUC Gapop 10.0,	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched: 1135193	11351937 seqs, 5372889281 residues
Total number of hits sat	Total number of hits satisfying chosen parameters: 22703874
Minimum DB seq length: 0 Maximum DB seq length: 200000000	0000000000
Post-processing: Minimum Match 08 Maximum Match 10 Listing first 45	Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: *

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AL057121 Drosophil				BG241147 OV1 38 G1			AL108460 Drosophil	AL393518 T7 end of	BG320266 Zm03 0340	AL537183 AL537183	AZ211117 SP_0159_B
SUMMARIES	CNS0057B	CNS014PA	BG786264	CNS0153F	BG241147	CNS02YYE	CNS0091P	CNS017SY	CNS06D94	BG320266	AL537183	AZ211117
DB	13	13	11	13	11	13	13	13	13	11	10	13
% Query Match Length DB 1	1014	1101	576	1101	520	848	925	1101	644	632	812	921
% Query Match	13.5	13.2	12.8	12.7	12.5	12.5	12.5	12.5	12.4	12.4	12.4	12.4
Score	61.2	9.69	58.2	57.4	56.8	9.95	56.4	56.4	56.2	26	26	26
Result No.	1	7	с С	47	5	9	c 2	8	6	10	c 11	c 12

55.8 12.3 892 13 AZ200928 55.4 12.2 566 13 CNS010RV 55.4 12.2 776 13 CNS010RV 55.4 12.2 848 13 CNS010RV 55.4 12.2 848 13 CNS010BA 55.4 12.2 848 13 CNS016BA 55.4 12.2 848 13 CNS006BA 55.4 12.1 878 13 CNS004NB 55.12.1 1016 11 BG7868339 54.8 12.1 1038 13 CNS004NB 55.12.1 1038 13 CNS004NB 54.4 12.0 651 11 BG7868339 54.4 12.0 651 11 BG786833 54.4 12.0 651 11 BG786804 53.6 11.8 895 13 AZ105894 53.6 11.8 895 13 AZ105894 53.6 11.8 895 13 CNS005NB 52.4 11.6 673 13 AZ185394 52.4 11.6 795 13 AZ185894 52.4 11.6 795 13 AZ185894 52.4 11.6 795 13 AZ185894 52.4 11.6 1016 13 CNS018NB 52.4 11.6 795 13 AZ185894 52.4 11.6 795 13 AZ185894 52.4 11.6 795 13 AZ185894 52.4 11.6 1016 13 CNS018NB 52.4 11.6 1016 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 915 13 AZ18517 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 1059 13 CNS018NB 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 1059 13 CNS018NB 52.2 11.5 915 13 AZ18516 52.2 11.5 915 13 AZ18517 52.2 11.5 910 6EVEY CEEX - FRANC - Web: www.genoscope. DIFFECT SUBMISSION SUBMITTED OF LIPE AT	AZ200928 SP_0134_B AZ196321 SP_1031_B AZ247077 Tetraodon AL099352 prosophil AL069031 prosophil AL064031 prosophil AL064031 prosophil BG36855 hVSME1002 BG786339 SEAUMC006 AL105973 prosophil BG411362 703709.x BG786337 SFAUMC006 AZ045300 prosophil BG076530 h3001005-AL066286 prosophil B09456 F26A17-Sp6 AL525224 AL525224 AL528524 AL525224 AL528678 Tetraodon AL066051 prosophil AZ188694 SP_1005_B	CNS015AB AL105197 Prosophil AZ184272 SP_1002_B AZ184272 SP_1002_B AZ184516 AZ184272 SP_1002_A AZ188516 AZ188474 SP_1012_A CNS02R43 AZ188474 SP_1012_A CNS03LU9 AL210108 Tetraodon CNS03LU9 AL24030 Tetraodon AZ195437 AL24030 Tetraodon AZ195437 AL26737 SP_1030_A AL581447 AL581447 AL581447 CNS0072Q AL06742 Drosophil AL1GNMENTS DNA GSS 03-JUN-1999 er genome survey sequence T7 end of BAC # 11brary from Drosophila melanogaster (fruit	Tracheata; Hexapoda; Insecta; philidae; Drosophila. pphilidae; Drosophila. ppe - Centre National de Sequencage: E (E-mail: seqref@enoscope.cns.fr. E (E-mail: seqref@enoscope.cns.fr. brosophila Genome Project (BDGP). ical map of the Drosophila shaCs. For further information .org The BDGP Drosophila epared by Kazutoyo Osoegawa and by a laboratory in the Department of Park Cancer Institute in Buffalo, Bark Cancer Institute in Buffalo, Etaliad description of the library the BACPAC Resource Center can be alo.edu/drosophila_bac.htm.
13 55.8 12.3 892 13 14 55.6 12.3 786 13 15 55.4 12.2 566 13 18 55.4 12.2 756 13 18 55.4 12.2 848 13 19 55.4 12.2 848 13 20 55.4 12.2 848 13 21 54.8 12.1 1016 13 22 54.8 12.1 878 13 23 54.4 12.0 651 13 24 12.0 651 13 25 54.2 12.0 745 13 26 53.6 11.8 699 10 31 53.2 11.7 794 13 32 53.6 11.8 895 13 33 52.4 11.6 791 13 34 52.2 11.5 925 13 35 52.4 11.6 795 13 36 52.4 11.6 795 13 37 52.2 11.5 925 13 38 52.4 11.6 795 13 39 52.4 11.6 795 13 31 52.2 11.5 925 13 42 52.2 11.5 925 13 42 52.2 11.5 925 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 46 52.2 11.5 1059 13 47 52.2 11.5 1059 13 48 52.2 11.5 1059 13 49 65.4 11.6 1014 bp 41 52.4 11.6 1014 bp 42 52.2 11.5 1059 13 43 52.2 11.5 1059 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 47 52.2 11.5 1059 13 48 52.2 11.5 1059 13 48 52.2 11.5 1059 13 49 65.5 11.5 1059 13 41 52.4 11.6 1014 bp 41 52.4 11.6 1014 bp 42 52.2 11.5 1059 13 43 52.2 11.5 1059 13 45 52.2 11.5 1059 13 45 52.2 11.5 1059 13 47 52.2 11.5 1059 13 48 52.2 11.5 1059 13 48 52.2 11.5 1059 13 49 65.5 10.0 00 00 00 00 00 00 00 00 00 00 00 00	AZ200928 AZ196321 CNS03JN0 CNS0118A CNS0118A CNS006B4 CNS006B4 CNS006B4 GG386625 BG386633 BG386633 BG78633 AZ194728 BG786337 AZ1952524 AZ194728 BG076530 AZ194728 BG076530 AZ194728 BG076530	ACMSO15AB AZ184272 AZ184272 AZ184272 AZ18474 CNSO3243 CNSO31U9 CNSO31U9 AZ195437 AL581447 AL581447 AL581447 AL581447 AL581447 AL581447 ALGNMENT ALIGNMENT ALIGNMENT ALIGNMENT ALIGNMENT ALIGNMENT	er Thhropoda: Tr Endopterygota dea: Drosophi ex: FRANCE (Cns: fr) BAC-end seque BAC-end seque BAC-end seque BAC-end seque BAC-end seque sing these BA W.fruitfly.or ary was prepa Ler de Jong's ary was prepa erer de Jong's ary was prepa A.fruitfly.or ary was prepa A.fruitfly.or ary was prepa A.fruitfly.or ary was prepa A.fruitfly.or ary was prepa A.fruitfly.or ary was prepa are de Jong's are Roswell Par ned RPCI-98 a Sosphila DNA A.fruitfly.or are prepaled and a prepaled a prepale
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13 55.8 14 55.6 15 55.4 17 55.4 18 55.4 19 55.4 19 55.4 19 55.4 22 20 55.4 23 54.4 24 25 54.4 25 24.2 26 53.6 31 53.2 32 52.4 41 52.4 41 52.4 41 52.4 41 52.4 42 52.2 44 52.2 45 52.4 41 52.4 41 52.4 41 52.4 42 52.2 44 52.2 45 52.4 41 52.4 41 52.4 41 52.4 42 52.2 44 52.2 45 52.2 46 52.2 47 52.2 48 52.2 48 52.2 49 52.4 41 52.4 41 52.4 41 52.4 42 52.2 44 52.2 45 52.2 46 52.2 47 52.2 48 52.2 48 52.2 49 52.4 40 52.2 41 52.4 41 52.4 42 52.2 44 52.2 45 52.2 46 52.2 47 52.2 48 52.2 48 52.2 49 52.2 49 52.2 40 52.2 40 52.2 40 52.2 41 52.2 42 52.2 43 60 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		11.6 11.6 11.6 11.6 11.6 11.5 11.5 11.5	17121.1 L F1y. Ophila Tyota; Yyota; Yyota; Yyota; Omorpha Omorpha Scope. Ct Subm Inted (91 9100 91 9100 91 9100 91 9100 91 10
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576 bp
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                                                                       Matches 136;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence "7 end of BAC BAC BACNIANIA of DrosBAC library from Drosophila melanogaster (fruit Liy), genomic survey sequence.
                                                                                                                                                                                                                                                                                 aagtggctacctgacccccaagt/gcgggccacctttgaagccgtgctagccaaactgg 313
                                                                                                                                                                                                                                                                                                                                                              MCMCMCCMCCCCCCGMCAACCCMYCCCCMGCMTMMCMCCGCCTMCCMMMCMCTC 343
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Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheala; Hexapoda; Inserta;
Pteryota; Neoptera; Endopteryoola; Diptera; Brachyera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                 Length 1014;
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/plasmid="pBeloBAC11"
                             melanogaster"
                                                                                                                                                             / Match 13.5%; Score 61.2; DB 13;
Local Similarity 35.9%; Pred. No. 0.014;
hes 99; Conservative 57; Mismatches 120;
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                         /organism="Drosophila m
/db_xref="taxon:7227"
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A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo.
Development 128 (2001) in press
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1. Charter 1 (bases 1 to 576)

2. Chur.X., Mahairas, G., 1111es, M.K., Cameron, R.A., Davidson, E.I.
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4400 Fitth Avenue, Pittsburgh, PA 15213, USA
17E1: ii 412 268 5849
Email: ettensohn∉andrew.emu.edu.
     DB 13;
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52; Mismatches 162;
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Drosophila melanogaster genome survey sequence 77 end of BAC
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/note="Organ: Mix of ovaries of varying immature stayes
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Fanicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 520)
Cordonnice Praff,M. M., Gingle,A., Marsala,C., Sudman,M. and Praft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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                                                                                         41 egeccacetycecycegeggtggatgletecaceegecaggeegaageegaageetger 100
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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
TTE: 706 542 1800
Fax: 706 542 1805
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                                                                                                                 ggetlacammigamigegetlinamigamachgaecgecaecqcaaccqcathaecmi
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    Length 1101;
                                               Indels
Score 57.4; DB 13;
Pred. No. 0.075;
25; Mismatches 188;
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/db_xref="taxon:4558"
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Contact: Cordonnier-Pratt MM
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12.78;
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSO2YYE 848 bp DNA GSS 15-MAY-2000
Terracdon nigroviridis genome survey sequence PUC-ori end of clone
181307 of library G from Tetracdon nigroviridis, genomic survey
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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodoniidae; Tetraodon.

I (bases 1 to 848)
Boses-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision." 23\ \rm c 113\ \rm g 59\ \rm t
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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Tetraodon nigroviridis DNA sequence
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                                                                                                                          Score 56.8; DB 11;
Pred. No. 0.093;
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48.5%;
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FEATURES

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Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY ccdex - FRANCE (E-mail : segref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitlly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="181J07"
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Pred. No. 0.1;
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EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - Intrp://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humanin) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence SP6 end of BACN37L08 of DrosBAC library from brosophila melanogaster (fruit Fly), genomic survey sequence.
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/organism="Drosophila melanogaster"
/dD_xref="texon:7227"
/clone_11b="RPCI-98"
/clone="BACR19D16"
/note="end: TET3"
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T7 end of clone ARGAAULDL2 of Library ARGAA from strain CBS 732
Zygosarcharomycus rouxil, qenomic survey sequence.
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de Montigny, J., Straub, M., Potier, S., Tekaia, F., Dujon, B., Wincker, P., Artiguenave, F. and Souciet, J.
Genomic exploration of the hemiascomycetous yeasts: 8.
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                                             /organism="Drosophila melanogaster"
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/clone="bBCN371.08"
/note="bacN371.08"
/note="wind: SP6"
1 a 176 c 160 y 152 r 359 ot!
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FEBS Lett. 487 (1), 52-55 (2000)
20584718
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                                                                               Direct Submission

M. Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

Seqreféqenoscope.cns: fr - Neb: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazii. Zygosaccharomyces rouxii,

lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
S. kb were prepared and both extremilites were sequenced. See
Reywords for description of this sequence and for the sequence of
the other extremity of this insert.
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1 (bases 1 to 632)
Simmonds,J.A., Singh,J.A., Piche,C., Cass,L., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 ctacacccgacggcgacctcaccgacaccgaacgcgcccgcaaacgcgcatcacctga 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 gccacctttgaagccgtgctagccaaactggccgccccggcgaccaaccccgacgac 342
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yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
20584711
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Pred. No. 0.12;
4; Mismatches 112;
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35.78;
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Best Local Similarity 35.7
Matches 92; Conservative
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/clone_lbb-"zm002_0
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Tags from Cold-Stressed Maize Seedlings Grown
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                         Under High Light Intensity
Unpublished (2001)
Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA OC6, Canada
Fax: (613) 759-1662
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AL537183 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS00F019YL14
prime, mKNA sequence.
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ed. No. 0.13;
Mismatches 166; Indels
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
Sequence Tags fro
Light Intensity
                                                                                                                                                                                                                                                                                                                                               Email: singhja@em.agr.ca
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Hes 137; Conservative
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gcaaccardacqqqctgctggccggqctgcqcgcgctg 450
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Pred. No. 0.14;
0; Mismatches 2
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California Institute of Technology
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                                                                                                                                                                                                                          Pasadena California 91125, USA
                                                                                                                                                                                                                                      Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 159 row: F column: 9
Seg primer: SP6
Class: BAC ends
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47.78;
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Matches 190; Conservative
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// Anote="Organ: Fetal brain; Vector: pcMVSPORT 6: 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I pcMVSPORT 6 vector. Library was constructed by Life Pechnologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville flang@lifetech.com URL :

http://fulllength.invitrogen.com"
                                                                                                                             /clone="CSOBF019YL14"
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/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: segreféquenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                   45 others
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                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 182;
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/organism="Strongylocentrotus purpuratus"
//dl_xref="taxon:7668"
//clone="Plate=150"
//clone=_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
//clone="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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                                                                                                  and
Strongylocentrotidae: Strongylocentrotus.

1 (bases 1 to 921)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. ar Hood, I.
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                                                                                                                                A sea urchin genome project: Sequence scan, virtual map, additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
Contact: Cameron, RA, Davidson, EH, Hood, L
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AZ196321 786 bp DNA GSS 31-AUG-2000 SP_1031_B2_D02_T7A Strongylocentrotus purpuratus, purple sea urchin sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-1031 Col-4 Kow-H, DNA sequence.
                                                                                                                                                                                                                                                                            1 (bases 1 to 786)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swattzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lohrach, H., Britten, R.J., Davidson, E.H. and Hood, L.
                                                                                                                                                                                                                                      Echinozoa;
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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                                                                                                                                                                                                           Strongylocentrolus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Eucchinoidea; Echinacea; Echinoida;
Strongylocentrolidae; Strongylocentrotus;
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Pred, No. 0.16;
0; Mismatches 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Division of Biology 156-29
California Institute of Technology
Basadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
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                                                                                                                                                                                             Strongylocentrotus purpuratus.
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Seq primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: acameron@caltech.edu
                                                                                                                                                         AZ196321.1 GF:8390144
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/organism="Strongylocentrotus purpuratus"

/db_xref="taxon:766"

/clone="Plate="134 Col=24 Row=F"

/clone="Plate="34 Col=24 Row=F"

/clone="1b="Strongylocentrotus purpuratus, purple sea

/rochin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli

DH10B"
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Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray
, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
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                                                                      Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinocea, Echinoida,
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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Division of Biology 156-29
California Institute of Technology
Passadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.3%; Score 55.8; DB 13;
llarity 46.0%; Pred. No. 0.15;
Conservative 0; Mismatches 222;
                                                                                                                              Strongylocentrotidae; Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 892.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: acameron@caltech.edu
Plate: 134 row: F column: 24
Seq primer: T7
                                                         Strongylocentrotus purpuratus.
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                     GI:8395946
                                                                                                                                                                                                                                                                                                                                                                                     Tel: (626) 395-8421
Fex: (626) 793-3047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends
 AZ200928
AZ200928.1
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                                                                                                                                               REFERENCE
                                                                                                                                                                 AUTHORS
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                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli ï 50 georgeograph grand glocosoco aggression as a second and consideration of the second contract of the second cont 110 cicaatairyteregaeggeggetggeeggetacgeecayegggieatggaetggetacare 169 ccgacggryacctcaccgacaccgaacgcgcccgcaaacgcgcatcacctgagcaacra 229 230 gcaatacgac-ggcatgtcacggctaagtggctacctgacccccaagtcgcgggccarc 288 349 coggicalinyacaccaccogatgoggoogceatogacogogacaccogoagcoaagin 408 Gaps

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GSS: genome survey sequence.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;

Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:

Actinopterygii: Neopterygii: Percomorpha; Tetracdontiformes;

Tetracdontidae; Tetracdon.

E 1 (bases 1 to 566)

S Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwarter pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                   566 bp DNA GSS 17-MAY-2000 nigroviridis genome survey sequence PUC-Ori end of clone library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using

Tetraodon nigroviridis DNA sequence
121 cccgacgagctggcccgctacgcccagcgggtcatggactggctacaccccgacggcgac 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ctcaccgacaccgaacgcgcccgcaaacgcgcatcaccctgagcaaccagcaatacgacg 240
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/db_xref="taxon:99883"
/db_xref="taxon:99883"
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/clone="lbb"G"
/note="Genoscope sequence ID : C0BG031DA02SP1-end
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AL247077.1 GI:7968089
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Best Local Similarity 39.8%
Matches 131; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                         Tetraodon 031B04 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope
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LOCUS
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VERSION
KEYWORDS
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AUTHORS
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